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116718

From: Hamud, Fozia
Sent: Thursday, March 11, 2004 12:54 PM
To: STIC-Biotech/ChemLib
Subject: search for 10/090,365

Kindly search SEQ ID NO: 48 of 10090,365 against commercial data bases and interference data bases. thanks.

Fozia Hamud
Patent Examiner
Art Unit 1647
Remsen, Room 4D70
Mail Box Remsen-4C70
272-0884

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STIC-BIOTECH DIVISION
(STIC)

Searcher: _____
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Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 116718

TO: Fozia Hamud
Location: REM/4D70/4C70
Art Unit: 1647
Monday, March 15, 2004
Case Serial Number: 10/090365

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Hamud,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2004, 15:55:02 ; Search time 60 Seconds
(without alignments)
1083.099 Million cell updates/sec

Title: US-10-090-365-48

Perfect score: 1242

Sequence: 1 MMPKCHLGLLIILLSSATE.....YQPMFRRSPRSKRCVHIP 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	230	5	Aae28616 Mouse Zcy
2	1234	99.4	230	5	Abj10501 Cytokine
3	1224	98.6	230	5	Aae28613 Mouse Zcy
4	831.5	66.9	231	5	Abj10510 Cytokine
5	829.5	66.8	231	5	Abj10514 Cytokine
6	827.5	66.6	231	5	Abj10519 Cytokine
7	826.5	66.5	231	4	Aae05048 Human ZCY
8	826.5	66.5	231	4	Aab62857 Human cyt
9	826.5	66.5	231	4	Aae02460 Human DNA
10	826.5	66.5	231	5	Aae28600 Human Zcy
11	826.5	66.5	231	5	Aae17320 Human cyt
12	826.5	66.5	231	5	Aae17381 Human cyt
13	826.5	66.5	231	5	Abj10498 Cytokine
14	826.5	66.5	231	5	Abg34086 Human Pro
15	826.5	66.5	231	5	Aae08000 Human IL-
16	826.5	66.5	231	6	Aae30826 Human cyt
17	826.5	66.5	231	6	Aae30838 Human cyt
18	826.5	66.5	231	6	Ada01382 Human PRO
19	826.5	66.5	231	6	Ada43811 Human sec
20	826.5	66.5	231	6	Ada43579 Human sec
21	826.5	66.5	231	6	Ada01254 Human PRO
22	826.5	66.5	231	7	Ada01138 Human sec
23	826.5	66.5	231	7	Ada43695 Human sec
24	826.5	66.5	231	7	Ada06957 Human PRO
25	826.5	66.5	231	7	Ada08445 Novel hum

26	826.5	66.5	231	7	ADB99738	Human PRO
27	826.5	66.5	231	7	ADB87021	Human PRO
28	826.5	66.5	231	7	ADB66176	Human sec
29	826.5	66.5	231	7	ADB99854	Human PRO
30	826.5	66.5	231	7	ADB99509	Novel hum
31	826.5	66.5	231	7	ADB66060	Human sec
32	826.5	66.5	231	7	ADC23458	Human tra
33	826.5	66.5	231	7	ADC26151	Human PRO
34	826.5	66.5	231	7	ADC04978	Human PRO
35	826.5	66.5	231	7	ADE11284	Human PRO
36	826.5	66.5	231	7	ADD88215	Human PRO
37	826.5	66.5	231	7	ADD95510	Human sec
38	826.5	66.5	231	7	ADE06440	Human PRO
39	826.5	66.5	231	7	ADD38215	Human PRO
40	826.5	66.5	231	7	ADD88331	Human PRO
41	826.5	66.5	231	7	ADD90912	Human sec
42	826.5	66.5	231	8	ADE51765	Human sec
43	826.5	66.5	231	8	ADE51881	Human sec
44	826.5	66.5	231	8	ADE37739	Human sec
45	826.5	66.5	231	8	ADE37623	Human sec

ALIGNMENTS

RESULT 1

AAE28616
ID AAE28616 standard; protein; 230 AA.

XX AAE28616;

AC AC

DT 27-DEC-2002 (first entry)

XX

DE Mouse Zcytor16 protein #2.

XX

KW Cytokine receptor; Zcytor16; IL-TiF; autoimmune disease; dermatological;
KW inflammatory disease; inflammatory bowel disease; rheumatoid arthritis;
KW asthma; systemic lupus erythematosus; myasthenia gravis; pancreatitis;
KW diabetes; atherosclerosis; glomerulonephritis; gene therapy; cytostatic;
KW immunosuppressive; nephrotropic; allergy; placental health; abortion;
KW cancer; mouse.
XX Mus musculus.

Key	Location/Qualifiers
Peptide	1..23
Protein	27..230
Domain	/label= Signal_peptide
Domain	/note= "Mouse mature Zcytor16 protein"
Domain	/note= "Cytokine binding domain"
Region	/note= "Fibronectin III domain I"
Domain	/note= "Linker"
Domain	/note= "Fibronectin III domain II"
Domain	/note= "Class II cytokine domain"

WO200270655-A2.

12-SEP-2002.

04-MAR-2002; 2002WO-US0006267.

02-MAR-2001; 2001US-0273035P.

27-MAR-2001; 2001US-0279232P.

(ZIMO) ZYMOGENETICS INC.

Presnell SR, Xu W, Kindsvogel W, Chen Z;

XX

DR WPI; 2002-598750/75.
XX N-PSDB; AAD45989.
XX New Zcytor16 polypeptide useful for treating autoimmune or inflammatory
PT diseases, e.g. inflammatory bowel disease, rheumatoid arthritis, asthma,
PT atherosclerosis, cancer or diabetes, or in assessing therapeutic aspects
PT of IL-TIF.
XX
XX
XX Claim 1; Page 219-220; 221pp; English.
XX
XX The invention relates to cytokine receptor designated as mouse Zcytor16
CC which can bind and antagonise the IL-TIF. The Zcytor16 polypeptide is
CC useful in modulating the immune system by binding Zcytor16 ligand, and
CC thus, preventing the binding of the ligand with endogenous Zcytor16
CC receptor. It is useful for studying human inflammation or immune
CC function, or for treating autoimmune or inflammatory diseases such as
CC inflammatory bowel disease, rheumatoid arthritis, asthma, systemic lupus
CC erythematosus, myasthenia gravis or allergy, atherosclerosis, cancer,
CC diabetes, glomerulonephritis or pancreatitis, or in assessing therapeutic
CC aspects of IL-TIF, chemical therapeutics, anti-IL-TIF antibodies, anti-
CC Zcytor16 antibodies or Zcytor16 soluble receptors. Zcytor16 DNA and the
CC anti-mouse Zcytor16 antibody are useful as probes in detecting gene
CC expression and gene structure, such as in the diagnosis and/or prevention
CC of spontaneous abortions or in monitoring placental health and function.
CC It is also used in gene therapy. The present sequence is mouse Zcytor16
CC protein
XX
XX Sequence 230 AA;

Query Match 100.0%; Score 1242; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 4e-127;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPKHCLGLLIILLSSATEIQPARVSLTPQKVFQSRNFHILHWQAGSSLPNNISYIF 60
Db 1 MNPKHCLGLLIILLSSATEIQPARVSLTPQKVFQSRNFHILHWQAGSSLPNNISYIF 60
QY 61 VOYKMYGQSQWEDKVCWGTTALFCDLTNETLDPYELYYGRVMTACAGHSAWTRTPRT 120
Db 61 VOYKMYGQSQWEDKVCWGTTALFCDLTNETLDPYELYYGRVMTACAGHSAWTRTPRT 120
QY 121 PWWETKLDPPVVTITRVNASLRVLLRPPELPNNQSGKNASMETYYGLVYRVFTINNSLE 180
Db 121 PWWETKLDPPVVTITRVNASLRVLLRPPELPNNQSGKNASMETYYGLVYRVFTINNSLE 180
QY 181 KEQKAYEGTORAVEIEGLIPHSYCVVVAEMYQPMFDRSPRSKERCCHIP 230
Db 181 KEQKAYEGTORAVEIEGLIPHSYCVVVAEMYQPMFDRSPRSKERCCHIP 230

RESULT 2
ABJ10501
ID ABJ10501 standard; protein; 230 AA.
XX
XX ABJ10501;
XX
XX 21-NOV-2002 (first entry)
XX
XX Cytokine receptor family 2 (CRF2) related protein SEQ ID No 12.
XX
XX Immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW anti-inflammatory; interleukin-antagonist-20; interferon-antagonist-22;
KW gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta;
KW interferon-antagonist-gamma; cytokine receptor family 2; CRF2-12;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW inflammation.
XX
XX Mus sp.
XX
XX WO200266647-A2.
XX
XX 29-AUG-2002.
XX

14-JAN-2002; 2002WO-US000986.
XX
XX 12-JAN-2001; 2001US-0261442P.
PR 06-FEB-2001; 2001US-0267021P.
PR 23-FEB-2001; 2001US-0270835P.
XX (GEMY) GENETICS INST LLC.
FA
XX Fouser L, Liu W, Deng B;
XX
XX WPI: 2002-674946/72.
DR N-PSDB; ABT08221.
XX
XX New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for
PT diagnosing and treating disorders with abnormal CRF2-12 activity such as
PT autoimmune diseases like rheumatoid arthritis, multiple sclerosis and
PT inflammation.
XX
XX Claim 12; Page 13; 91pp; English.
XX
XX The invention relates to an isolated type 2 cytokine receptor family
CC (CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids
CC 21-66 of a 231 residue amino acid sequence, given in the specification,
CC or its complement. The compositions and methods of the present invention
CC are useful for diagnosing, screening and treating disorders associated
CC with abnormal CRF2-12 activity such as autoimmune diseases like
CC rheumatoid arthritis, multiple sclerosis and inflammation. This sequence
CC represents a cytokine receptor family 2 (CRF2-12) protein relating to the
CC invention
XX
XX Sequence 230 AA;

Query Match 99.4%; Score 1234; DB 5; Length 230;
Best Local Similarity 99.6%; Pred. No. 3e-126;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNPKHCLGLLIILLSSATEIQPARVSLTPQKVFQSRNFHILHWQAGSSLPNNISYIF 60
Db 1 MNPKHCLGLLIILLSSATEIQPARVSLTPQKVFQSRNFHILHWQAGSSLPNNISYIF 60
QY 61 VOYKMYGQSQWEDKVCWGTTALFCDLTNETLDPYELYYGRVMTACAGHSAWTRTPRT 120
Db 61 VOYKMYGQSQWEDKVCWGTTALFCDLTNETLDPYELYYGRVMTACAGHSAWTRTPRT 120
QY 121 PWWETKLDPPVVTITRVNASLRVLLRPPELPNNQSGKNASMETYYGLVYRVFTINNSLE 180
Db 121 PWWETKLDPPVVTITRVNASLRVLLRPPELPNNQSGKNASMETYYGLVYRVFTINNSLE 180
QY 181 KEQKAYEGTORAVEIEGLIPHSYCVVVAEMYQPMFDRSPRSKERCCHIP 230
Db 181 KEQKAYEGTORAVEIEGLIPHSYCVVVAEMYQPMFDRSPRSKERCCHIP 230

RESULT 3
AAE28613
ID AAE28613 standard; protein; 230 AA.
XX
XX AAE28613;
XX
XX 27-DEC-2002 (first entry)
XX
XX Mouse Zcytor16 protein #1.
XX
XX Cytokine receptor; Zcytor16; IL-TIF; autoimmune disease; dermatological;
KW inflammatory disease; inflammatory bowel disease; rheumatoid arthritis;
KW asthma; systemic lupus erythematosus; myasthenia gravis; pancreatitis;
KW diabetes; atherosclerosis; glomerulonephritis; gene therapy; cytostatic;
KW immunosuppressive; nephrotropic; allergy; placental health; abortion;
KW cancer; mouse.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers

Peptide 1. .23
/label= Signal_peptide
Protein 24. .230
/note= "Mouse mature Zcytor16 protein"
Domain 31. .229
/note= "Cytokine binding domain"
Domain 31. .122
/note= "Fibronectin III domain I"
Region 123. .130
/note= "Linker"
Domain 131. .229
/note= "Fibronectin III domain II"
Domain 219. .222
/note= "Class II cytokine domain"
WO200270655-A2.
12-SEP-2002.
04-MAR-2002; 2002WO-US006267.
02-MAR-2001; 2001US-0273035P.
27-MAR-2001; 2001US-0279232P.
(Zymo) ZYMOGENETICS INC.
Presnell SR, Xu W, Kindsvogel W, Chen Z;
WPI; 2002-698750/75.
N-PSDS; AAD45982.
New Zcytor16 polypeptide useful for treating autoimmune or inflammatory diseases, e.g. inflammatory bowel disease, rheumatoid arthritis, asthma, atherosclerosis, cancer or diabetes, or in assessing therapeutic aspects of IL-TIF.
Claim 1; Page 213; 221pp; English.
The invention relates to cytokine receptor designated as mouse Zcytor16 which can bind and antagonise the IL-TIF. The Zcytor16 polypeptide is useful in modulating the immune system by binding Zcytor16 ligand, and thus, preventing the binding of the ligand with endogenous Zcytor16 receptor. It is useful for studying human inflammation or immune function, or for treating autoimmune or inflammatory diseases such as inflammatory bowel disease, rheumatoid arthritis, asthma, systemic lupus erythematosus, myasthenia gravis or allergy, atherosclerosis, cancer, diabetes, glomerulonephritis or pancreatitis, or in assessing therapeutic aspects of IL-TIF, chemical therapeutics, anti-IL-TIF antibodies, anti-Zcytor16 antibodies or Zcytor16 soluble receptors. Zcytor16 DNA and the anti-mouse Zcytor16 antibody are useful as probes in detecting gene expression and gene structure, such as in the diagnosis and/or prevention of spontaneous abortions or in monitoring placental health and function. It is also used in gene therapy. The present sequence is mouse Zcytor16 protein
Sequence 230 AA;
Query Match 98.6%; Score 1224; DB 5; Length 230;
Best Local Similarity 99.1%; Pred. No. 3.7e-125; Indels 0; Gaps 0;
Matches 228; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MNPKHCLGLLIIILSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSIYF 60
Db 1 MNPKHCLGLLIIILSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSIYF 60
Qy 61 VOYKXMGOSQWEDKVDGWTGTTALFCDLTNETLDPYELYYGRVMTACAGHSAMTRPRF 120
Db 61 VOYKXMGOSQWEDKVDGWTGTTALFCDLTNETLDPYELYYGRVMTACAGHSAMTRPRF 120
Qy 121 PWWETKLDPPVVTITRVNASLRVLLRPPELPRNQSGKNASMETYYGLVYRVFTINNSL 180
Db 121 PWWETKLDPPVVTITRVNASLRVLLRPPELPRNQSGKNASMETYYGLVYRVFTINNSL 180

Qy 181 KEQKAYECTQRAVEIEGLIPHSYCVVAEMTQPMFDRSPRSKERCWIP 230
Db 181 KEQKAYECTQRAVEIEGLIPHSYCVVAEMTQPMFDRSPRSKERCWIP 230
RESULT 4
ID ABJ10510 standard; protein; 231 AA.
AC ABJ10510;
XX 21-NOV-2002 (first entry)
XX Cytokine receptor family 2 (CRF2) related protein SEQ ID No 21.
XX Immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
XX antinflammatory; interleukin-antagonist-20; interleukin-antagonist-22;
XX gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta;
XX interferon-antagonist-gamma; cytokine receptor family 2; CRF2-12;
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis;
XX inflammation.
XX Unidentified.
XX WO200266647-A2.
XX 29-AUG-2002.
XX 14-JAN-2002; 2002WO-US000986.
XX 12-JAN-2001; 2001US-0261442P.
XX 06-FEB-2001; 2001US-0267021P.
XX 23-FEB-2001; 2001US-0270835P.
XX (GEMY) GENETICS INST LLC.
XX Fouser L, Liu W, Deng B;
XX WPI; 2002-674946/72.
XX New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for
XX diagnosing and treating disorders with abnormal CRF2-12 activity such as
XX autoimmune diseases like rheumatoid arthritis, multiple sclerosis and
XX inflammation.
XX Example 11; Page 78; 91pp; English.
XX The invention relates to an isolated type 2 cytokine receptor family
XX (CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids
XX 21-66 of a 231 residue amino acid sequence, given in the specification,
XX or its complement. The compositions and methods of the present invention
XX are useful for diagnosing, screening and treating disorders associated
XX with abnormal CRF2-12 activity such as autoimmune diseases like
XX rheumatoid arthritis, multiple sclerosis and inflammation. This sequence
XX represents a cytokine receptor family 2 (CRF2-12) protein relating to the
XX invention
XX Sequence 231 AA;
Query Match 66.9%; Score 831.5; DB 5; Length 231;
Best Local Similarity 67.1%; Pred. No. 3.4e-82;
Matches 155; Conservative 20; Mismatches 55; Indels 1; Gaps 1;
Qy 1 MNPKHCLGLLIIILSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSIY 59
Db 1 MNPKHCLGLLIIILSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSIY 60
Qy 60 FVOYKXMGOSQWEDKVDGWTGTTALFCDLTNETLDPYELYYGRVMTACAGHSAMTRPRF 119
Db 61 FVOYKXMGOSQWEDKVDGWTGTTALFCDLTNETLDPYELYYGRVMTACAGHSAMTRPRF 120
Qy 120 TPWWETKLDPPVVTITRVNASLRVLLRPPELPRNQSGKNASMETYYGLVYRVFTINNSL 179
Db 120 TPWWETKLDPPVVTITRVNASLRVLLRPPELPRNQSGKNASMETYYGLVYRVFTINNSL 179

Db 121 TPWETKIDPPVNMITQVNGSLVILHAPNLPYQKKNVSIEDYVYLLYRVFIINNSL 180
QY 180 EKEQKAYEQTQRAVEIEGLIPHSSYCVVAEMYPQWEDRSPSKERCVCVHIP 230
Db 181 EKEQKAYEQAHRVAIEALTPHSSYCVVAETIYQPMIDRRSQSERCVCVEIP 231

RESULT 5
ID ABJ10514
XX ABJ10514 standard; protein; 231 AA.
AC ABJ10514;
XX
DT 21-NOV-2002 (first entry)
XX
DE Cytokine receptor family 2 (CRF2) related protein SEQ ID No 25.
XX
KW Immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; interleukin-antagonist-20; interleukin-antagonist-22;
KW gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta;
KW interferon-antagonist-gamma; cytokine receptor family 2; CRF2-12;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW inflammation.
XX
OS Unidentified.
XX
PN WO200266647-A2.
XX
PD 29-AUG-2002.
XX
PF 14-JAN-2002; 2002WO-US000986.
XX
PR 12-JAN-2001; 2001US-0261442P.
XX
PR 06-FEB-2001; 2001US-0267021P.
XX
PR 23-FEB-2001; 2001US-0270835P.
XX
PA (GEMY) GENETICS INST LLC.
XX
PI Fouser L, Liu W, Deng B;
XX
PI WPI; 2002-674946/72.
XX
DR
XX
PT New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for
PT diagnosing and treating disorders with abnormal CRF2-12 activity such as
PT autoimmune diseases like rheumatoid arthritis, multiple sclerosis and
PT inflammation.
XX
PS Example 15; Page 79; 91pp; English.
XX
CC The invention relates to an isolated type 2 cytokine receptor family
CC (CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids
CC 21-66 of a 231 residue amino acid sequence, given in the specification,
CC or its complement. The compositions and methods of the present invention
CC are useful for diagnosing, screening and treating disorders associated
CC with abnormal CRF2-12 activity such as autoimmune diseases like
CC rheumatoid arthritis, multiple sclerosis and inflammation. This sequence
CC represents a cytokine receptor family 2 (CRF2-12) protein relating to the
CC invention
XX
SQ Sequence 231 AA;
Query Match 66.8%; Score 829.5; DB 5; Length 231;
Best Local Similarity 67.1%; Pred. No. 5.6e-82;
Matches 155; Conservative 19; Mismatches 56; Indels 1; Gaps 1;

QY 1 MNPKHCLGLLI-ILLSSATEIQPARVSLTPQKRVQSRNFHNLHWQAGSLPNNISY 59
Db 1 MNPKHCFGLGFLISFFLTGVAGTQSTHESLKPQKRVQSRNFHNLQWQGRALTGNSSVY 60
QY 60 FVQYKYGQSQWEDKVDGCTTALFCDLTNETLDPYELLYGVRMTACAGHSAWTETPRF 119
Db 61 FVQYKYGQSQWEDKVDGCTTALFCDLTNETLDPYELLYGVRMTACAGHSAWTETPRF 120

QY 120 TPWETKIDPPVNMITQVNGSLVILHAPNLPYQKKNVSIEDYVYLLYRVFIINNSL 179
Db 121 TPWETKIDPPVNMITQVNGSLVILHAPNLPYQKKNVSIEDYVYLLYRVFIINNSL 180
QY 180 EKEQKAYEQTQRAVEIEGLIPHSSYCVVAEMYPQWEDRSPSKERCVCVHIP 230
Db 181 EKEQKAYEQAHRVAIEALTPHSSYCVVAETIYQPMIDRRSQSERCVCVEIP 231

RESULT 6
ID ABJ10519
XX ABJ10519 standard; protein; 231 AA.
AC ABJ10519;
XX
DT 21-NOV-2002 (first entry)
XX
DE Cytokine receptor family 2 (CRF2) related protein SEQ ID No 30.
XX
KW Immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; interleukin-antagonist-20; interleukin-antagonist-22;
KW gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta;
KW interferon-antagonist-gamma; cytokine receptor family 2; CRF2-12;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW inflammation.
XX
OS Unidentified.
XX
PN WO200266647-A2.
XX
PD 29-AUG-2002.
XX
PF 14-JAN-2002; 2002WO-US000986.
XX
PR 12-JAN-2001; 2001US-0261442P.
XX
PR 06-FEB-2001; 2001US-0267021P.
XX
PR 23-FEB-2001; 2001US-0270835P.
XX
PA (GEMY) GENETICS INST LLC.
XX
PI Fouser L, Liu W, Deng B;
XX
PI WPI; 2002-674946/72.
XX
DR
XX
PT New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for
PT diagnosing and treating disorders with abnormal CRF2-12 activity such as
PT autoimmune diseases like rheumatoid arthritis, multiple sclerosis and
PT inflammation.
XX
PS Example 20; Page 81; 91pp; English.
XX
CC The invention relates to an isolated type 2 cytokine receptor family
CC (CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids
CC 21-66 of a 231 residue amino acid sequence, given in the specification,
CC or its complement. The compositions and methods of the present invention
CC are useful for diagnosing, screening and treating disorders associated
CC with abnormal CRF2-12 activity such as autoimmune diseases like
CC rheumatoid arthritis, multiple sclerosis and inflammation. This sequence
CC represents a cytokine receptor family 2 (CRF2-12) protein relating to the
CC invention
XX
SQ Sequence 231 AA;
Query Match 66.8%; Score 827.5; DB 5; Length 231;
Best Local Similarity 67.1%; Pred. No. 9.2e-82;
Matches 155; Conservative 19; Mismatches 56; Indels 1; Gaps 1;

QY 1 MNPKHCLGLLI-ILLSSATEIQPARVSLTPQKRVQSRNFHNLHWQAGSLPNNISY 59
Db 1 MNPKHCFGLGFLISFFLTGVAGTQSTHESLKPQKRVQSRNFHNLQWQGRALTGNSSVY 60
QY 60 FVQYKYGQSQWEDKVDGCTTALFCDLTNETLDPYELLYGVRMTACAGHSAWTETPRF 119

Db 61 FVOYKIYQORQWKNKDCWGTQELSCDLTSETSDIQEPYIGRVRAASAGSYSEWSMTPRF 120
QY 120 TPWETKLDPPVVTITRVNASLVLRLPPELPNRNSQGNASMETYYGLVYRVFTINNSL 179
Db 121 TPWETKIDPPVPMNITQVNGSLVLHAPNLPYQYQKEKNVSIEDYVELLYRVFIINNSL 180
QY 180 EKEQKAYEGTORAVEIEGLIPHSSYCVVAEMYPQMFDRSPRSKERCVCVHIP 230
Db 181 EKEQKAYEGTORAVEIEGLIPHSSYCVVAEMYPQMFDRSPRSKERCVCVHIP 231
RESULT 7
AAE05048
ID AAE05048 standard; protein; 231 AA.
XX
AC AAE05048;
DT 10-SEP-2001 (first entry)
XX
DE Human ZCYTO18 soluble receptor antagonist, zcytor16 protein.
XX
KW Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
KW cancer; inflammation; gene therapy; zcytor16.
XX
OS Homo sapiens.
XX
PN WO200146422-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US035308.
XX
PR 23-DEC-1999; 99US-00471767.
PR 01-DEC-2000; 2000US-0250841P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kindsvogel W;
XX
XX WPI: 2001-408548/43.
DR N-PSDB; AAB09745.
XX
PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer.
XX
PS Example 13A; Page 158-159; 167pp; English.
XX
CC The patent discloses novel human cytokine, ZCYTO18 protein and its
CC corresponding DNA. ZCYTO18 protein induces proliferation of cells
CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity in
CC K562 cells. ZCYTO18 DNA is useful for detecting a genetic abnormality in
CC a patient. ZCYTO18 DNA and its antibodies are useful for detecting cancer
CC and inflammation. ZCYTO18 protein is useful for killing cancer cells. It
CC is useful for increasing platelets in a patient or injured tissue. It is
CC also used in gene therapy. The present sequence is human zcytor16, which
CC is a naturally expressed soluble receptor antagonist of ZCYTO18 protein
XX
SQ Sequence 231 AA;
Query Match 66.5%; Score 826.5; DB 4; Length 231;
Best Local Similarity 66.7%; Pred No. 1.2e-81;
Matches 134; Conservative 20; Mismatches 56; Indels 1; Gaps 1;
QY 1 MNPKHCLGLLI-ILSSATEIPQARVSTPQKVFQGRNFHNLHWAGSLPNNIY 59
Db 1 MNPKHCLGLISFLTGVAGTQSTHESLKQVQFQSRNFHNLQWPGRALTGNSVY 60
QY 60 FVOYKMGYQOSQWEDKVDGTTALFCDLTNETLDPVELYGRVMTACGRHSWTRPRF 119
Db 61 FVOYKIYQORQWKNKDCWGTQELSCDLTSETSDIQEPYIGRVRAASAGSYSEWSMTPRF 120
QY 120 TPWETKLDPPVVTITRVNASLVLRLPPELPNRNSQGNASMETYYGLVYRVFTINNSL 179
Db 121 TPWETKIDPPVPMNITQVNGSLVLHAPNLPYQYQKEKNVSIEDYVELLYRVFIINNSL 180

QY 180 EKEQKAYEGTORAVEIEGLIPHSSYCVVAEMYPQMFDRSPRSKERCVCVHIP 230
Db 181 EKEQKAYEGTORAVEIEGLIPHSSYCVVAEMYPQMFDRSPRSKERCVCVHIP 231
RESULT 8
AAB62657
ID AAB62657 standard; protein; 231 AA.
XX
AC AAB62657;
DT 23-JUL-2001 (first entry)
XX
DE Human cytokine receptor, zcytor16.
XX
KW Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;
KW antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic;
KW immunosuppressive; chromosome 9q24.1-25.2; human.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Domain 22..231
FT /note= "extracellular domain"
FT Domain 22..108
FT /note= "Ig domain 1"
FT Domain 112..210
FT /note= "Ig domain 2"
XX
PN WO200140467-A1.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032703.
XX
PR 03-DEC-1999; 99US-0169049P.
PR 13-SEP-2000; 2000US-0232219P.
PR 31-OCT-2000; 2000US-0244610P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Presnell SR, Xu W, Kindsvogel W, Chen Z;
XX WPI: 2001-356158/37.
DR N-PSDB; AAF83735.
XX
CC New soluble cytokine receptor polypeptides and polynucleotides, useful
CC for diagnosing and treating cancer and inflammatory conditions.
XX
XX Claim 1; Page 186-188; 210pp; English.
CC The invention relates to a human cytokine receptor polypeptide,
CC designated zcytor16. The zcytor16 polypeptide can be expressed by
CC standard recombinant methodology and can bind to IL-TIF (undefined). The
CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC or differentiation of hematopoietic cell(s) (progenitors); reducing IL-
CC TIF induced or IL-9 induced inflammation; and suppressing an inflammatory
CC response in a mammal with inflammation. Heteromeric/ multimeric receptor
CC polypeptides such as soluble zcytor 16/CRP2-4 can be used to reduce
CC progression and symptoms of cancer. Zcytor16 polypeptides can also be
CC used to detect IL-TIF levels which is indicative of pathological
CC conditions including inflammatory states (e.g. rheumatoid arthritis) and
CC cancer. Antibodies that bind zcytor16 polypeptides and the polypeptides
CC themselves are useful for the treatment of inflammation, inflammatory
CC diseases (e.g. infection, asthma, inflammatory bowel disease, rheumatoid
CC arthritis and atherosclerosis) and autoimmune diseases. The antibodies
CC and zcytor16 polynucleotides are also useful for detecting cancer. The
CC present sequence represents the human zcytor16 protein
XX
SQ Sequence 231 AA;
Query Match 66.5%; Score 826.5; DB 4; Length 231;

Best Local Similarity 66.7%; Pred. No. 1.2e-81; Mismatches 20; Conservative 154; Indels 1; Gaps 1;

QY 1 MPMKCHLLGLLI-ILLSSATEIQPARVSLTPQKRVQSRNFHNLHWAQSSLPNNISY 59
DB 1 MPMKCHFLGLISFFLTGVAGTQSTHESLKPVQVQSRNFHNLHWAQSGRALTGNSSVY 60
QY 60 FVQYKMGQSQWEDKVDGWTGTTALFCDLTNETLDPYLYYGRVMTACAGHSATWTPRF 119
DB 61 FVQYKIYQQRQWKNKEDCWGTQELSCDLTSETSDIQEPPYGRVRAASAGSYSEWSMTPRF 120
QY 120 TPWETKLDPPVVTITRVNASLRLVLRPPPELNRNOSGKNASMETYYGLVYRVFTINNSL 179
DB 121 TPWETKIDPPVNNITQVNGSLVLHAPNLPYRQKEKVSIEDYVYLLRVFIINNSL 180
QY 180 EKEQAYEGTORAVEIEGLIPHSYCVVAEMYPQMFDRSPRSKRCVHIP 230
DB 181 EKEQVYEGAHRAVEIEALTPHSSYCVVAEIQPMLDRRSQRSERCVEIP 231

RESULT 9
AAE02460
ID AAE02460 standard; protein; 231 AA.
AC AAE02460;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human DNAX cytokine receptor subunit 4.2 (DCRS4.2).
XX
XX Human; immunomodulator; DNAX cytokine receptor subunit 4.2; DCRS4.2;
KW therapy; immunological disorder; drug screening; cell development;
XX chromosome 6q24.1-25.2.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= Signal-peptide
FT Protein 22..231
FT /label= DCRS4.2
FT /note= "Human mature DNAX cytokine receptor subunit 4.2"
XX
PN WO200136467-A2.
XX
XX 25-MAY-2001.
XX
XX 16-NOV-2000; 2000WO-US031363.
XX
XX 18-NOV-1999; 99US-00443060.
XX
XX 13-DEC-1999; 99US-0170320P.
XX
XX (SCHE) SCHERING CORP.
XX
XX Gorman DM;
XX
XX WPI; 2001-343800/36.
XX
XX N-PSDB; AAD06414.
XX
XX New mammalian receptor proteins related to cytokine receptors, useful for
XX regulating cell development and for diagnosis and treatment of
XX immunological disorders.
XX
XX Claim 3; Page 23; 124pp; English.
XX
XX The present sequence is human DNAX cytokine receptor subunit 4.2
XX (DCRS4.2). DCRS4 gene is located on chromosome 6q24.1-25.2. Cytokine
XX receptors, fragments and antibodies are useful for treating immunological
XX disorders. DCRS3 (5OR), DCRS4 (cytor) or fragments are useful in drug
XX screening to identify compounds having binding affinity to the receptor
XX subunit. Modulators of DCRS are useful for modulating the physiology or
XX development of a cell or tissue culture cells. A purified DCRS is useful
XX as a reagent to detect antibodies generated in response to the presence

CC of elevated levels of expression, or immunological disorders which lead
CC to production of antibody to the endogenous receptor. Cytokine receptor
CC sequences are useful as probes for detecting levels of the cytokine
CC receptor in patients suspected of having an immunological disorder.
CC Antibodies have therapeutic value, are useful as potent antagonist, in
CC detecting or quantifying ligands, for isolating DCRS proteins and
CC peptides, to screen expression libraries for particular expression
CC products, to raise anti-idiotypic antibodies and for detecting or
CC diagnosing various immunological conditions related to expression of the
XX protein or cells which express the protein

QY Sequence 231 AA;

Query Match 66.5%; Score 826.5; DB 4; Length 231;
Best Local Similarity 66.7%; Pred. No. 1.2e-81;
Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;

QY 1 MPMKCHLLGLLI-ILLSSATEIQPARVSLTPQKRVQSRNFHNLHWAQSSLPNNISY 59
DB 1 MPMKCHFLGLISFFLTGVAGTQSTHESLKPVQVQSRNFHNLHWAQSGRALTGNSSVY 60
QY 60 FVQYKMGQSQWEDKVDGWTGTTALFCDLTNETLDPYLYYGRVMTACAGHSATWTPRF 119
DB 61 FVQYKIYQQRQWKNKEDCWGTQELSCDLTSETSDIQEPPYGRVRAASAGSYSEWSMTPRF 120
QY 120 TPWETKLDPPVVTITRVNASLRLVLRPPPELNRNOSGKNASMETYYGLVYRVFTINNSL 179
DB 121 TPWETKIDPPVNNITQVNGSLVLHAPNLPYRQKEKVSIEDYVYLLRVFIINNSL 180
QY 180 EKEQAYEGTORAVEIEGLIPHSYCVVAEMYPQMFDRSPRSKRCVHIP 230
DB 181 EKEQVYEGAHRAVEIEALTPHSSYCVVAEIQPMLDRRSQRSERCVEIP 231

RESULT 10
AAE28600
ID AAE28600 standard; protein; 231 AA.
AC AAE28600;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human Zcytor16 protein.
XX

Cytokine receptor; Zcytor16; IL-TIF; autoimmune disease; dermatological;
inflammatory disease; inflammatory bowel disease; rheumatoid arthritis;
asthma; systemic lupus erythematosus; myasthenia gravis; pancreatitis;
diabetes; atherosclerosis; glomerulonephritis; gene therapy; cytostatic;
immunosuppressive; nephrotropic; allergy; placental health; abortion;
cancer; human; chromosome 6.

OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..22
FT /label= Signal_peptide
FT Protein 23..231
FT /note= "Mouse mature Zcytor16 protein"
FT Domain 32..230
FT /note= "Cytokine binding domain"
FT Domain 32..123
FT /note= "Fibronectin III domain I"
FT Region 124..131
FT /note= "Linker"
FT Domain 132..230
FT /note= "Fibronectin III domain II"
FT Domain 220..223
FT /note= "Class II cytokine domain"

PN WO200270655-A2.
XX
XX 12-SEP-2002.
XX

PF 04-MAR-2002; 2002WO-US006267.
XX
PR 02-MAR-2001; 2001US-0273035P.
PR 27-MAR-2001; 2001US-0279232P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Xu W, Kindsvogel W, Chen Z;
XX
DR WPI; 2002-698750/75.
DR N-PSDB; AAD45959.
XX
XX New Zcytor16 polypeptide useful for treating autoimmune or inflammatory
PT diseases, e.g. inflammatory bowel disease, rheumatoid arthritis, asthma,
PT atherosclerosis, cancer or diabetes, or in assessing therapeutic aspects
PT of IL-TIF.
XX
XX
PS Example 1; Page 191; 221pp; English.
XX
XX The invention relates to cytokine receptor designated as mouse Zcytor16
CC which can bind and antagonise the IL-TIF. The Zcytor16 polypeptide is
CC useful in modulating the immune system by binding Zcytor16 ligand, and
CC thus, preventing the binding of the ligand with endogenous Zcytor16
CC receptor. It is useful for studying human inflammation or immune
CC function, or for treating autoimmune or inflammatory diseases such as
CC inflammatory bowel disease, rheumatoid arthritis, asthma, systemic lupus
CC erythematosus, myasthenia gravis or allergy, atherosclerosis, cancer,
CC diabetes, glomerulonephritis or pancreatitis, or in assessing therapeutic
CC aspects of IL-TIF, chemical therapeutics, anti-IL-TIF antibodies, anti-
CC Zcytor16 antibodies or Zcytor16 soluble receptors. Zcytor16 DNA and the
CC anti-mouse Zcytor16 antibody are useful as probes in detecting gene
CC expression and gene structure, such as in the diagnosis and/or prevention
CC of spontaneous abortions or in monitoring placental health and function.
CC It is also used in gene therapy. The present sequence is human Zcytor16
CC protein. Human Zcytor16 gene resides at chromosome 6
XX
XX Sequence 231 AA;
XX
Query Match 66.5%; Score 826.5; DB 5; Length 231;
Best Local Similarity 66.7%; Pred. No. 1.2e-81;
Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;
QY 1 MNPKECLGLII-ILLSSATEIQPARVSLTPKQRFQSRNFHNLHWAGSLPSNNISY 59
DB 1 MNPKECFGLFLISPLTGVAGTQSTHESLKQRFQSRNFHNLHWQPGRLTGNSSVY 60
QY 60 FVQYRWYQSQWEDKVDGCTGTTALFCDLTNETLDPYELLYGRVMTACGRHSAMTRPRF 119
DB 61 FVQYKIYQQRQWKNEDCWGTQSLTSETSDIQEYGRVRAASAGSYSEWSMTPRF 120
QY 120 TPWWTKIDPPVVTITRNASLRLVLRPELPRNOSGKNASMETYYGLVYRVFTINNSL 179
DB 121 TPWWTKIDPPVPMNITQVNGSLVLVILHAPNUPYRYQKEKNVSIEDYYELLYRVFIINNSL 180
QY 180 EKEQKAYGTQRAVIEGLIPSHSYCVVAEMVQPMFDRSRKRCVHIP 230
DB 181 EKEQKVGAGRAVIEALTPSHSYCVVAEIQPMLDRRSQSRSERCVIEP 231
XX
RESULT 11
ID AAE17320
XX AAE17320 standard; protein; 231 AA.
XX
AC AAE17320;
XX
XX
DT 18-APR-2002 (first entry)
XX
DE Human cytokine receptor protein, sbg456548CytoRa #2.
XX
XX Human; therapy; wound healing disorder; vaccine; cancer; infection;
KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
KW multiple sclerosis; Alzheimer's disease; analgesic; cardiac; asthma;
KW

KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
KW depression; cardiovascular disease; myocardial infarction; renal failure;
KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
KW hyperplasia; renal disease; hypoglycaemia; gastrointestinal disease;
KW neutropenic; Hodgkin's disease; neuroleptic; anti-inflammatory;
KW haemostatic; vulvovaginitis; anticonvulsant; antirheumatic; neuroprotective;
KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebrotropic;
KW allergy; cytokine receptor.
XX
XX Homo sapiens.
XX
XX WO200198342-A1.
XX
XX 27-DEC-2001.
XX
XX 22-JUN-2001; 2001WO-US019929.
XX
XX 22-JUN-2000; 2000US-0213156P.
XX 22-JUN-2000; 2000US-0213161P.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX (GLAXO) GLAXO GROUP LTD.
XX
XX Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA, Xie Q, Rizni SK;
XX Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
XX WPI; 2002-139783/18.
XX N-PSDB; AAD27815.
XX
XX Novel secreted and membrane-associated polypeptides and polynucleotides
PT useful for preventing, ameliorating or correcting dysfunction or disease
PT including diabetes, cancer, hypertension and growth abnormalities.
XX
XX Claim 1; Page 132-133; 138pp; English.
XX
XX The invention relates to secreted and membrane-associated polypeptides
CC and polynucleotides. The sequences of the invention are useful in
CC diagnostic assays for detecting diseases associated with inappropriate
CC activity or levels of these polynucleotides, and in identifying their
CC agonists and antagonists that are potentially useful in therapy. The
CC sequences of the invention are useful as vaccines for inducing
CC immunological response. The sequences of the invention are useful for
CC treating cancers, infections, autoimmune disorders, haematopoietic
CC disorders, wound healing disorders, cholesterol ester storage disease,
CC inflammation, congenital muscular dystrophy, functional epidermolysis
CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
CC allergies, schizophrenia, sbg442445PROA-associated disorders,
CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,
CC graft versus host disease, ischaemia, stroke, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
CC depression, anxiety disorders and sleep disorders, cardiovascular
CC diseases including congestive heart failure and myocardial infarction,
CC respiratory diseases including chronic obstructive pulmonary disease,
CC acute bronchitis and adult respiratory distress syndrome, liver disorders
CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
CC and non-viral hepatitis, type II diabetes mellitus, renal disease
CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
CC and tendinitis, gastrointestinal diseases including intestinal
CC obstruction and tropical sprue, spleen disorders including hypersplenism,
CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
CC reproductive diseases including low testosterone and male infertility.
XX The present sequence is human cytokine receptor
XX
XX Sequence 231 AA;
XX
Query Match 66.5%; Score 826.5; DB 5; Length 231;
Best Local Similarity 66.7%; Pred. No. 1.2e-81;
Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;
XX

Matches	154;	Conservative	20;	Mismatches	56;	Indels	1;	Gaps	1;
QY	1	MMPKCHLLGLLI	-ILLSSATETQPARVSLTPQKVFQSFQSFNFHILHWQAGSSLPNSNIY	59					
DB	1	MMPKCHFLGLISFFLTIVAGTQSTHESLKPQRQVFQSFQSFNFHILQWPGHALTGNSSVY	60						
QY	60	FVQYKMYGQSQWEDKVDCKGTTFALPCDLLNETLDPYELYGRVMTACAGRHSAWTRTPRF	119						
DB	61	FVQYKIYQGRQWKNKEBCWGTQELSCDLFTSETSDIQEPYGRVRAASAGSYSEWSMTPRF	120						
QY	120	TPPWETKLDPVVTITRIVNASLVLRLRPPELPNRSQSGKNASMETYGLGVYRVFTINSL	179						
DB	121	TPPWETKLDPVNNITQVNGSLVLILHANLPYRQKEQVSIEDYELLVYRVFIINSL	180						
QY	180	EKEQKAYEGTQRAVEIEGLPHSSYCVVAEMTQPMFDRRSRPSKRCVHIP	230						
DB	181	EKEQKYVEGAHRAVEIATLPHSSYCVVAEIIYCPMLDRRSORSSERCVVEIP	231						

RESULT 13	
ABU10498	
ID	ABU10498 standard; protein; 231 AA.
XX	
XX	ABU10498;
XX	
DT	21-NOV-2002 (first entry)
XX	
XX	Cytokine receptor family 2 (CRF2) related protein SEQ ID No 2.
XX	
XX	Immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW	antiinflammatory; interleukin-antagonist-20; interleukin-antagonist-22;
KW	gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta;
KW	interferon-antagonist-gamma; cytokine receptor family 2; CRF2-12;
KW	autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW	inflammation.
XX	
XX	Unidentified.
OS	
DE	WO200266647-A2.
PN	
XX	
PD	29-AUG-2002.
XX	
XX	14-JAN-2002; 2002WO-US000986.
PF	
XX	
XX	12-JAN-2001; 2001US-0261442P.
PR	06-FEB-2001; 2001US-0267021P.
PR	23-FEB-2001; 2001US-0270835P.
XX	
XX	(GEMY) GENETICS INST LLC.
PA	
XX	
PI	Fouser L, Liu W, Deng B;
XX	
XX	WPI; 2002-674946/72.
DR	N-PSDB; ABT08216.;
DR	
XX	
PT	New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for
PT	diagnosing and treating disorders with abnormal CRF2-12 activity such as
PT	autoimmune diseases like rheumatoid arthritis, multiple sclerosis and
PT	inflammation.
XX	
XX	Claim 2; Page 6; 91pp; English.
PS	
XX	
CC	The invention relates to an isolated type 2 cytokine receptor family
CC	(CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids
CC	21-66 of a 231 residue amino acid sequence, given in the specification,
CC	or its complement. The compositions and methods of the present invention
CC	are useful for diagnosing, screening and treating disorders associated
CC	with abnormal CRF2-12 activity such as autoimmune diseases like
CC	rheumatoid arthritis, multiple sclerosis and inflammation. This sequence
CC	represents a cytokine receptor family 2 (CRF2-12) protein relating to the
CC	invention
XX	
SQ	Sequence 231 AA;

DR	XX	Query Match	66.5%; Score 826.5; DB 5; Length 231;	
PT	XX	Best Local Similarity	66.7%; Pred. No. 1.2e-81;	
PT	XX	Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;		
PS	XX	1 MWPKECHLLGLLI-ILLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSIY 59		
XX	XX	1 MWPKECHFLGLISFFLTGVAGTQSTHESLXKQRFQSRNFHNLQWQPGALTCNSSVY 60		
CC	CC	60 FVOYKMGQSQWEDKVDGCTTALFCDLTNETLDPYELLYGRVMTACAGHSAWTRPRF 119		
CC	CC	61 FVOYKIYQGRQWKNKEDCWGTQELSCDLTSETSDIQEPYIGRVRAASAGSYSEWSMTPRF 120		
CC	CC	120 TPWETKLDPPVVTITRVNASLRVLLRPPLEPNRQSGKNASMETYYGLVYRVFTINNSL 179		
CC	CC	121 TPWETKIDPPVMNITQVNGSLLVILHAFNLPYRYQKEKNVSIEDYELLYRVFTINNSL 180		
CC	CC	180 EKEQKAYEGTQRAVEIEGLIPHSYCVVAEMYPQMFDRRSPRSKRCVHIP 230		
CC	CC	181 EKEQKVEGAHRAVEIEALTPHSSYCVVAETIQPMLDRRSQSEERCVEIP 231		
CC	CC	RESULT 14		
CC	CC	ABG34086		
ID	XX	ABG34086 standard; protein; 231 AA.		
AC	XX	ABG34086;		
XX	XX	15-JUL-2002 (first entry)		
XX	XX	Human Pro peptide #57.		
XX	XX	Human; PRO; secreted protein; transmembrane protein; genetic disorder;		
XX	XX	tumour; cancer.		
XX	XX	Homo sapiens.		
XX	XX	WO200224898-A2.		
XX	XX	28-MAR-2002.		
XX	XX	29-AUG-2001; 2001WO-US027099.		
XX	XX	01-SEP-2000; 2000US-022989EP.		
XX	XX	05-SEP-2000; 2000US-0230621P.		
XX	XX	22-SEP-2000; 2000US-0235147P.		
XX	XX	10-NOV-2000; 2000WO-US030873.		
XX	XX	12-JAN-2001; 2001US-0261878P.		
XX	XX	16-JAN-2001; 2001US-0261910P.		
XX	XX	16-JAN-2001; 2001US-0261939P.		
XX	XX	16-JAN-2001; 2001US-0262150P.		
XX	XX	25-JAN-2001; 2001US-0264395P.		
XX	XX	02-FEB-2001; 2001US-0266421P.		
XX	XX	09-FEB-2001; 2001US-0267623P.		
XX	XX	28-FEB-2001; 2001WO-US006520.		
XX	XX	03-MAR-2001; 2001US-0274399P.		
XX	XX	03-APR-2001; 2001US-0280982P.		
XX	XX	04-APR-2001; 2001US-0282129P.		
XX	XX	04-APR-2001; 2001US-0282199P.		
XX	XX	09-MAY-2001; 2001US-0290589P.		
XX	XX	25-MAY-2001; 2001WO-US017092.		
XX	XX	01-JUN-2001; 2001WO-US017800.		
XX	XX	20-JUN-2001; 2001WO-US019692.		
XX	XX	29-JUN-2001; 2001WO-US021066.		
XX	XX	09-JUL-2001; 2001WO-US021735.		
XX	XX	(GETH) GENENTECH INC.		
XX	XX	Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;		
XX	XX	Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;		
XX	XX	Fong S;		
XX	XX	WPI; 2002-362426/39.		
DR	XX			
DR	XX	Query Match	66.5%; Score 826.5; DB 5; Length 231;	
DR	XX	Best Local Similarity	66.7%; Pred. No. 1.2e-81;	
DR	XX	Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;		
DR	XX	1 MWPKECHLLGLLI-ILLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSIY 59		
DR	XX	1 MWPKECHFLGLISFFLTGVAGTQSTHESLXKQRFQSRNFHNLQWQPGALTCNSSVY 60		
DR	XX	60 FVOYKMGQSQWEDKVDGCTTALFCDLTNETLDPYELLYGRVMTACAGHSAWTRPRF 119		
DR	XX	61 FVOYKIYQGRQWKNKEDCWGTQELSCDLTSETSDIQEPYIGRVRAASAGSYSEWSMTPRF 120		
DR	XX	120 TPWETKLDPPVVTITRVNASLRVLLRPPLEPNRQSGKNASMETYYGLVYRVFTINNSL 179		
DR	XX	121 TPWETKIDPPVMNITQVNGSLLVILHAFNLPYRYQKEKNVSIEDYELLYRVFTINNSL 180		
DR	XX	180 EKEQKAYEGTQRAVEIEGLIPHSYCVVAEMYPQMFDRRSPRSKRCVHIP 230		
DR	XX	181 EKEQKVEGAHRAVEIEALTPHSSYCVVAETIQPMLDRRSQSEERCVEIP 231		
DR	XX	RESULT 15		
DR	XX	AAU80000		
DR	XX	ID AAU80000 standard; protein; 231 AA.		
DR	XX	AAU80000;		
DR	XX	15-JUL-2002 (first entry)		
DR	XX	Human IL-TIF/IL-22 binding protein #1.		
DR	XX	Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;		
DR	XX	IL-TIF/IL-22 antagonist.		
DR	XX	Homo sapiens.		
DR	XX	WO200224912-A2.		
DR	XX	28-MAR-2002.		
DR	XX	21-SEP-2001; 2001WO-US029576.		
DR	XX	22-SEP-2000; 2000US-0234583P.		

PR 03-NOV-2000; 2000US-0245495P.
PR 31-JUL-2001; 2001US-00919182.
XX (LUDW-) LUDWIG INST CANCER RES.
FA
XX
XX Renauld J, Dumoutier L;
XX
XX WPI; 2002-383190/41.
DR N-PSDB; ABK50076.
XX
XX Polynucleotide and polypeptide of soluble protein which binds to
PT interleukin-Tif/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a
PT cell.
XX
XX
PS Claim 14; Page 39; 42pp; English.
XX
XX The present invention relates to a new polynucleotide that encodes a
CC soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred
CC to as IL-22BP), where the complementary sequence of the invention
CC hybridises under stringent conditions to a nucleotide sequence of 2271 or
CC 2366 base pairs, as given in the specification. The molecules of the
CC invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22
CC on a cell, for determining whether IL-TIF/IL-22 is present in a sample,
CC for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably
CC in vitro, and for obtaining an antibody molecule specific for the soluble
CC binding protein of the invention, from a population or panel of antibody
CC molecules of diverse binding specificity. The soluble protein is further
CC useful in manufacture of a medicament for treating an IL-22 mediated
CC disease and for assaying an agent, preferably an antibody or a peptide
CC fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding
CC of the soluble protein to IL-TIF/IL-22, where the agent identified is
CC used in the manufacture of medicament for treating IL-TIF/IL-22 mediated
CC disorder. The antibody is useful for determining presence of the soluble
CC protein, where the antibody is detectably labelled. The present amino
CC acid sequence represents the human IL-TIF/IL-22 binding protein #1 of the
XX invention
SQ Sequence 231 AA;
Query Match 56.5%; Score 826.5; DB 5; Length 231;
Best Local Similarity 86.7%; Pred. No. 1.2e-81;
Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;
Qy 1 MMPKHCLLGLLI-ILLSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSLPSNNSIY 59
Db 1 MMPKHCFGLFLISGFLTGAGTQSTHESLKPQVQFQSRNFHNLQWQGRALTGNSSVY 60
Qy 60 FVQYKMYQSQWEDKVDGCTTALFCDLTNETLDPYELVYGYMTACAGHSAWTTPTTF 119
Db 61 FVQYKIYQKQWKNKEDCWGTQELSCDLTSETSDIQEPIYGRVRAASAGSIENSWTPTTF 120
Qy 120 TPWWETKLDPPVVTITRVNASRLVLLRPPELPNRNQSGKNASMETYGLVYRVFTINNSL 179
Db 121 TPWWETKIDPPVNNITQVNGSLLVILHAPNLPYRYQKKNVSIEDYVELLYRVFIINNSL 180
Qy 180 EKEQKAYEGTORAVEIEGLIPHSYCVVAEMYQPMDFRSPRSKRCVHIP 230
Db 181 EKEQKVEGAHRAVEIEALTFHSYCVVAETIYQPMLDLDRSRSEERCVEIP 231

Search completed: March 12, 2004, 15:58:07
Job time : 62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: March 12, 2004, 15:56:57 ; Search time 20 Seconds
(without alignments)
1106.203 Million cell updates/sec

Title: US-10-090-365-48
Perfect score: 1242
Sequence: 1 MPKHCILGLLIILSSATE.....YQMFDRSPRSKRCVHIP 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pirl1.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	174.5	14.0	575	A49667	interleukin-10 rec
2	174.5	14.0	578	I56215	interleukin-10 rec
3	173	13.9	349	JC6311	interferon recepto
4	165.5	13.3	489	A31555	interferon gamma r
5	153	12.3	325	A47003	cytokine receptor
6	150	12.1	292	1 KFB03	tissue factor prec
7	145.5	11.7	295	1 KFB03	tissue factor prec
8	144.5	11.6	292	1 KFB3	interferon alpha/b
9	140	11.3	590	A45283	tissue factor prec
10	138.5	11.2	294	1 KFB3	interferon gamma r
11	138.5	11.2	477	A34368	interferon alpha r
12	134.5	10.8	560	S37387	interferon alpha/b
13	123.5	9.9	331	A54295	interferon recepto
14	123.5	9.9	331	S59501	interferon alpha-b
15	122.5	9.9	515	I39073	interferon alpha/b
16	120.5	9.7	557	A32694	interferon gamma r
17	110	8.9	337	I38500	interferon gamma r
18	99	8.0	2029	1 TDFLX	protein-tyrosine-p
19	95.5	7.7	332	A49947	interferon gamma r
20	93	7.5	272	JQ1802	B8R 31K protein pr
21	93	7.5	1607	T43212	insulin-like growt
22	92	7.4	266	I36855	gene B9R protein -
23	92	7.4	272	G42526	B8R protein - vacc
24	91.5	7.4	379	T19773	hypothetical prote
25	90	7.2	266	T28607	hypothetical prote
26	90	7.2	266	T28607	H9R protein - vari
27	87.5	7.0	562	C72278	hypothetical prote
28	85.5	6.9	202	H69495	conserved hypothet
29	85.5	6.9	263	A44229	interferon-gamma r

30	84.5	6.8	1443	2	I50600	neogenin - chicken
31	81.5	6.6	674	2	A47222	Kallmann syndrome
32	81.5	6.6	676	2	B47222	Kallmann syndrome
33	81.5	6.6	792	2	SI6880	ribonucleoside-dip
34	81.5	6.6	1209	2	T42718	probable neural ce
35	81.5	6.6	1608	1	WMTGM	interleukin-3 rece
36	81	6.5	896	2	I56563	interleukin-3 rece
37	81	6.5	1375	2	T13822	frazzled gene prot
38	81	6.5	1526	2	T13823	frazzled gene prot
39	80.5	6.5	566	2	T46159	cytochrome P450-1i
40	80.5	6.5	1256	2	T03096	CDO protein - rat
41	80	6.4	335	2	T49145	hypothetical prote
42	80	6.4	703	2	T41065	RNA binding protei
43	79.5	6.4	359	2	JC7280	cytokine receptor
44	79.5	6.4	1240	2	T03097	CDO protein - huma
45	79	6.4	1825	2	C88400	protein H19M22.1 [

ALIGNMENTS

RESULT 1

A49667
interleukin-10 receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2000
C/Accession: A49667
R;Ho, A.S.; Liu, Y.; Khan, T.A.; Hau, D.H.; Bazar, J.F.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993
A>Title: A receptor for interleukin 10 is related to interferon receptors.
A/Reference number: A49667; MUID:94068585; PMID:8248239
A/Accession: A49667
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-575 <RES>
A/Cross-references: GB:L12120; NID:G437615; PIDN:AAA16156.1; PID:G437616
C/Genetics:
A/Gene: IL10R
C/Superfamily: interleukin-10 receptor IL10R
C/Keywords: cytokine receptor

Query Match	14.0%	Score	174.5	DB	2	Length	575
Best Local Similarity	29.6%	Pred. No.	9.1e-09				
Matches	73	Conservative	35	Mismatches	92	Indels	47
Gaps	15						
QY	7	LLGLLILLSSATEIQPARVSI	TPQKVFQSFNFHILHMQAGSSLP	--SNNSIYFYQY	63		
Db	5	LLPFLVTLSSLEFIAYGTLPSPSYVWFARFQHLHWK	---PINQSESTIYEVAL	61			
QY	64	KMYGOSMEDKVDGCGTTALFCDLTNETLDPYELYYG	---RVMTACAGRHSAWTRT	-PRP	119		
Db	62	KQYGSTWNDIHCRAQALSCLTFTLDLYHRSYGYRARVRAVDNSQYSNWTTTTRF	121				
QY	120	TPWETKLDPPVVTITRYNASILVJ	-----LRPELPNRSQGNKASMETIYGLVY	--	170		
Db	122	T-----VDEVILTVDVS	--LUKAMDGIYGTIHPPR	-PTTPAGDE	-----YQVFKD	166	
QY	171	-RVFTINNSLEKEQKAYEGTQRAVE	-----IEGLIPHSYCVVVAEMYQPMFDRSPR	---S	222		
Db	167	LAVYKI--SIRFSELKNATKRVKQETTLTPIGVKRFV	---KVLPRLESINKAEMS	221			
QY	223	KRCVHI	229				
Db	222	EEQCLLI	228				

RESULT 2

I56215
interleukin-10 receptor - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2000
C/Accession: I56215
R;Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore, K.W.

J. Immunol. 152, 1821-1829, 1994
A/Title: Expression cloning and characterization of a human IL-10 receptor.
A/Reference number: I56215; MUID:94165477; PMID:8120391
A/Accession: I56215
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-578 <RES>
A/Cross-references: EMBL:U00672; NID:9482802; PIDN:AAAI7896.1; PID:9482803
C/Genetics:
A/Genes: GDB:IL10R; HIL-10R
A/Cross-references: GDB:330958; OMIM:146933
A/Map position: 11q23.3-11q23.3
C/Superfamily: interleukin-10 receptor IL10R
C/Keywords: cytokine receptor

Query Match 14.0%; Score 174.5; DB 2; Length 578;
Best Local Similarity 28.7%; Pred. No. 9.2e-09;
Matches 72; Conservative 37; Mismatches 95; Indels 47; Gaps 15;

QY 1 MNPKHLLGLLLISL-----SATEIQPARVSLTPQKVRFSQRNFHNLHQAGSLP 53
Db 1 MNP-CLVLLAALLSLRGLSDAHGTLP-----SPSPVWEAEFFHHILHW---TIP 49
QY 54 --SNNSIYVQVMYQSQWEDKVDGTTALFCDLTNETLDPYEL--YGRVMTACAGR 109
Db 50 NOSESTCYEALLRYGIESWNSISNC--SQTLSYDLTAVTLDYHNSGYRVRVADGSR 107
QY 110 HSAWTRT-PRFTPMWETKLDPPVITIRVNASLR--VLLRPPELNRSQSGKNASMETTY 166
Db 108 HSNWTVNTRFS-----VDEVLTVGSVNLHNGFILGKQLPRPKMAPANDYEIF 161
QY 167 GLVYRVFTINNSLEKQAYEQTAVEIEGLIPHS-----YCVVAEMYQPMFRRSPR 221
Db 162 S-HFREYEI--AIRKVPNGFTTHKKVGHENFSLTSGEVGFCV---QVKPSVASRSNK 215
QY 222 ---SKERCVHI 229
Db 216 GMSKCECISL 226

RESULT 3
JC6311
C/Species: Mus musculus (house mouse)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
R/Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A/Title: CRF2-4: Isolation of cDNA clones encoding the human and mouse proteins.
A/Reference number: JC6311; MUID:97199375; PMID:9047351
A/Accession: JC6311
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-349 <GIB>
A/Cross-references: GB:U53696

Query Match 13.9%; Score 173; DB 2; Length 349;
Best Local Similarity 27.8%; Pred. No. 6.7e-09;
Matches 64; Conservative 32; Mismatches 94; Indels 40; Gaps 12;

QY 6 CLIGLL--IILLSSATEIQPARVSLTPQKVRFSQRNFHNLHQAGSLSPNSIYFVQY 63
Db 4 CVAGLWGLFLVPALGMIPP-----PEKVRMNSVNFKNILQWEV-PAPFKTNLTATQY 56
QY 64 KMYQSQWEDKVDGTTALFCDLTNETLDPYELYYGRVMTACAGRHSAWTRTPFTPMW 123
Db 57 ESRVSFQ----DHCKRTASTQCDFSH--LSKYGDYIVRVRAELADEHSWNVV-rFCPVE 109
QY 124 ETKLDPVWITIRVNASLRVLLRPPELNRSQSG--KNASMETTYGLVYRV-FTINNSLE 180
Db 110 DTIIGPEMQIESLAESLELRFAPQIENEPETWLNK-----IYDSWAYRVQVWKNGTNE 165
QY 181 KEQ--KAYEQTAVEIEGLIPHSYCV-----VAEMYQPMFDR 217

Db 166 KFOVSPYD-----SEVIRNLEFWTTICIQVQGLLDQNRIGSESPICER 211

RESULT 4
A31555
interferon gamma receptor precursor - human
C/Species: Homo sapiens (man)
C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999
C/Accession: A31555
R/Aguet, M.; Dembic, Z.; Merlin, G.
Cell 55, 273-280, 1988
A/Title: Molecular cloning and expression of the human interferon-gamma receptor.
A/Reference number: A31555; MUID:89003065; PMID:29711451
A/Accession: A31555
A/Molecule type: mRNA
A/Residues: 1-489 <AGU>
A/Cross-references: GB:J03143; NID:gi84650; PIDN:AAAS2731.1; PID:g306915
C/Genetics:
A/Genes: GDB:IFNGR1; IFNGR
A/Cross-references: GDB:1120688; OMIM:107470
A/Map position: 6q23-6q24
C/Superfamily: interferon gamma receptor
C/Keywords: cytokine receptor; transmembrane protein

Query Match 13.3%; Score 165.5; DB 2; Length 489;
Best Local Similarity 24.6%; Pred. No. 5.5e-08;
Matches 60; Conservative 47; Mismatches 108; Indels 29; Gaps 10;

QY 7 LLGLLILLSSATEIQPARVSL-----TPQKVRFSQRNFHNLHW--QAGSSLPSNNSI 58
Db 3 LLFLLPLVMGVRAEMGTADLPSSVPFTNTVIESYNNPIVYWEYQIMPQVP---V 58
QY 59 YFVQYKMYG--QSQWEDKVDGTTALFCDLTNETLDPYELYYGRVMTACAGRHSAWTRT 116
Db 59 FTVEVKYGVKNGSEWIDA--CINISHHYCNISDHVGDPNSLWVRVKARVGQKESAYAKS 116
QY 117 PRFTPMWETKLDPPVITIRVNASLRV--LLRPPELNRSQSGKNASME-TYYGLVYRVFT 174
Db 117 EEFVAVCRDGGIKGPPKLDIRKEKQIWDIFHPBSVFNVDGEQVDYDPTTCIRVNVYV 176
QY 175 INNSLEKEQKAYEGTQR-----AVEIEGLIP-----HSSYCVVAEMYQPMFDRRSPSKER 225
Db 177 RMNGSEIQYKIL--TKEDDCDEIQQLAIPVSSLSNQYCVSAEGLVHVGVTTEKSEV 234
QY 226 CVHI 229
Db 235 CITI 238

RESULT 5
A47003
cytokine receptor family class II protein CRF2-4 precursor - human
C/Species: Homo sapiens (man)
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 01-Dec-2000
C/Accession: A47003; G01418
R/Lutfalla, G.; Gardiner, K.; Uze, G.
Genomics 16, 366-373, 1993
A/Title: A new member of the cytokine receptor gene family maps on chromosome 21 at les:
A/Reference number: A47003; MUID:93300510; PMID:8314576
A/Accession: A47003
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-325 <LUT>
A/Cross-references: GB:217227; NID:g3933378; PIDN:CAA78933.1; PID:g3933379
R/Lutfalla, G.
submitted to the EMBL Data Library, April 1994
A/Reference number: G06935
A/Accession: G01418
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-123, 'D', 125-268, 'VGRME', <LU2>
A/Cross-references: EMBL:U08986; NID:g571295; PID:g571296

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;Genetics:
;Gene: GDB:CRFB4; CRF2-4
;Cross-references: GDB:138168; OMIM:123889
;Map position: 21q; 21q22.1-21q22.2
;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
;Keywords: transmembrane protein

Query Match      12.3%; Score 153; DB 2; Length 325;
Best Local Similarity 27.2%; Pred. No. 5.3e-07;
Matches 61; Conservative 29; Mismatches 96; Indels 38; Gaps 10;

2Y 14 LLSSATEIQPARVSLTPQKVFQSRFNHILHWQAGSSLPNNNSIYFVQYKMGQSQWED 73
2b 13 LLVSALGWVP-----PPNVNNSVNFKNILQWES-PATAKGNLTATQYLSY-RIFQD 64
2Y 74 KVCWGTTALFCDLTNETLDPYLYGYRVMTACAGRHSAWTRPTPWETKLDPEVVT 133
2b 65 K-CMNTLTTECDFS--SLSKYGDHLTRVRAEFADEHSDWVNI-TFCPVDVDTIIGPGNQ 119
2Y 134 ITRVNASLRVLLAPPELPNRNQG--KNASMETVYGLVYRVFTNNLSLEKEQKAYEGTQR 191
2b 120 VEVLADSLHWRFLAPKTIENYEYETWTKN-----VNSWTYNYQYWK-----NGTDE 165
2Y 192 AVET-----EGLPHPSYCVAAEMYPMDRRSPRSKERC 226
2b 166 KFQITPOYDFEVLRLNLEPWITTCYQVRGFLPDRNKAGEWSEPYC 209

RESULT 6
CP03
Tissue factor precursor - bovine
;Alternate names: coagulation factor III
;Species: Bos primigenius taurus (cattle)
;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
;Accession: JQ1319
;Takayenoki, Y.; Mura, T.; Miyata, T.; Iwanaga, S.
Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991
A>Title: cDNA and amino acid sequences of bovine tissue factor.
A'Reference number: JQ1319; MUID:92109720; PMID:1764065
A'Accession: JQ1319
A'Molecule type: mRNA
A'Residuals: 1-292 <TAK>
A'Cross-references: GB:S74147; NID:G241438; PIDN:AB20755.1; PID:G241439
A'Experimental source: adrenal gland
A'Note: part of this sequence, including the amino end of the mature protein, was confir
C'Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C'Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C'Superfamily: tissue factor
C'Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
F.1-35/Domain: signal sequence #status predicted <SIG>
F.36-292/Product: tissue factor #status experimental <MAT>
F.36-248/Domain: extracellular #status predicted <EXT>
F.249-271/Domain: transmembrane #status predicted <TM>
F.272-292/Domain: intracellular #status predicted <INT>
F.43.153.181/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.81-89.215-238/Disulfide bonds: #status predicted
F.118.124/Binding site: carbohydrate (Thr) (covalent) #status predicted
F.274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match      12.1%; Score 150; DB 1; Length 292;
Best Local Similarity 24.9%; Pred. No. 8.9e-07;
Matches 60; Conservative 47; Mismatches 90; Indels 44; Gaps 13;

QY 7 LLGLLIL---LSSATEIQPARVSLTPQKVFQSRFNHILHWQAGSSLPNNNSIYFVQY 63
Db 21 LFLGLIIGAGVAGTVD-----VAINITKSTNFKTILEWEP-----KPINHYTVQI 70
QY 64 KMGQSQWEDKVCWGTTALFCDLTNETLDPYLYGYRVMTACAGRHSA-----WTRTP 117
Db 71 SP-RLGNKKNK--CFYTTNTECDVTDTEIKVNVRETYLARVLSYADTSSTVPEPFTNSP 127
QY 118 RPTPWETKLDPEVVTI-----TRVNASL---RVLLRPE--LPNRQSGKNASMETVY 167
;Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane

Db 128 EFTPLYETNLQOPTIQSFQVGTGKLVNTVQDARTLVANSFAFLSLRDVFGKDLNLYLYW 187
QY 168 LVYRVFTNNLSLEKEQKAYEGTQRAVEIEGLIPHSSYC--VVAEMYPMDRRSPRSKER 225
Db 188 KA-----SSTGKKKATTNTNGFLIDVD---KGENYCFHVQAVILSRVNRQKSPSPSPK 237
QY 226 C 226
Db 238 C 238

RESULT 7
KFHUS
Tissue factor precursor [validated] - human
;Alternate names: coagulation factor III
;Species: Homo sapiens (man)
;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Dec-2000
;Accession: A43645; A47574; A28320; A29672; A29008
R.Mackman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.
Biochemistry 28, 1755-1762, 1989
A>Title: Complete sequence of the human tissue factor gene, a highly regulated cellular
A'Reference number: A43645; MUID:89247359; PMID:2719931
A'Accession: A43645
A'Molecule type: DNA
A'Residuals: 1-295 <MAC>
A'Cross-references: GB:J02846; NID:G339505; PIDN:AAA61152.1; PID:G339506
R.Fisher, K.L.; Gorman, C.M.; Vehar, G.A.; O'Brien, D.P.; Lawn, R.M.
Thromb. Res. 48, 89-99, 1987
A>Title: Cloning and expression of human tissue factor cDNA.
A'Reference number: A47574; MUID:88100453; PMID:3424286
A'Accession: A47574
A'Molecule type: mRNA
A'Residuals: 1-295 <FIS>
A'Cross-references: GB:M27436; NID:G339507; PIDN:AAA36734.1; PID:G339508
R.Spicer, E.K.; Horton, R.; Bloom, L.; Bach, R.; Williams, K.R.; Guha, A.; Kraus, J.; Li
Proc. Natl. Acad. Sci. U.S.A. 84, 5148-5152, 1987
A>Title: Isolation of cDNA clones coding for human tissue factor: primary structure of t
A'Reference number: A94171; MUID:87260946; PMID:3037536
A'Accession: A28320
A'Molecule type: mRNA
A'Residuals: 1-295 <SPI>
A'Cross-references: GB:J02931; NID:G339501; PIDN:AAA61150.1; PID:G339502
R.Morrissey, J.H.; Fakhrai, H.; Edgington, T.S.
Cell 50, 129-135, 1987
A>Title: Molecular cloning of the cDNA for tissue factor, the cellular receptor for the
A'Reference number: A29062; MUID:87244317; PMID:3297348
A'Accession: A29062
A'Molecule type: mRNA
A'Residuals: 1-295 <MOR>
A'Cross-references: GB:J02931; NID:G339501; PIDN:AAA61150.1; PID:G339502
A'Note: part of this sequence, including the amino end of the mature protein, was confir
R.Scarpati, E.M.; Wen, D.; Broze Jr., G.J.; Milelich, J.P.; Flandermeyer, R.R.; Siegel,
Biochemistry 26, 5234-5238, 1987
A>Title: Human tissue factor: cDNA sequence and chromosome localization of the gene.
A'Reference number: A29672; MUID:88050796; PMID:2823875
A'Accession: A29672
A'Molecule type: mRNA
A'Residuals: 1-259, 'A', 261-295 <SCA>
A'Cross-references: GB:M1653; NID:G339503; PIDN:AAA61151.1; PID:G339504
R.Bach, R.; Konigsberg, W.H.; Nemersohn, Y.
Biochemistry 27, 4227-4231, 1988
A>Title: Human tissue factor contains thioester-linked palmitate and stearate on the cyt
A'Reference number: A37422; MUID:8900804; PMID:3166978
A'Contents: annotation; disulfide bonds and fatty acid binding site
C'Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor
C'Comment: Expression of tissue factor can be induced in a variety of tissues by certain
C'Genetics:
A'Gene: GDB:F3
A'Cross-references: GDB:119895; OMIM:134390
A'Map position: 1p22-1p21
A'Introns: 34/1; 71/2; 138/1; 197/3; 251/1
C'Superfamily: tissue factor
C'Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane
```


QY	68	OSQWEDKVDGWTGTTALFCDLTNETL--DPYELYVGRVMT-----ACAGRHSA	112
DB	69	RN--WKK--CFSTIDTECDLTDLVQDVTWAYEAKVLSVPRNSVHGDGDLVIHGEERP	125
QY	113	WTRTRPTPMTWKLPDPV-----TITRVNASLRVLLRPPELPNPN	154
DB	126	FTNAPKFLPYRDTNLGQPIVQFEQDGRKLVNVVVDLSLTVLRKNGTFLTL-----RQ	177
QY	155	OSGNASMETVYGLVYRFTINNSLEKEQKAYEGTORAVEIEGLIPLHSYVC--VVAEMVQ	212
DB	178	VFGDLG-----YITVRK---GSTGKKTITNTNFSIDVEGV---SYCFVQAMIFS	227
QY	213	PMFDRRSPRSKERC	226
DB	228	RKTQNSPFGSSTVC	241
RESULT 11			
DB	A34368	interferon gamma receptor precursor - mouse	
C:Species: Mus musculus (house mouse)			
C>Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 23-Jul-1999			
C:Accession: A34368; A34568; A34423; A34508; A36224; I48941			
J:Kumar, C.S.; Muchukumaran, G.; Frost, L.J.; Nee, M.; Ahn, Y.H.; Mariano, T.M.; Pestka, R. Biol. Chem. 264, 17939-17945, 1989			
A:Title: Molecular characterization of the murine interferon gamma receptor cDNA.			
A:Reference number: A34368; MUID:90036866; PMID:2530216			
A:Accession: A34368			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-477 <KUM>			
A:Cross-references: GB:M25764; NID:G197962; PIDN:AAA39177.1; PID:G309393			
J:Cofano, F.; Moore, S.K.; Tanaka, S.; Yuhki, N.; Landolfo, S.; Appella, E. J. Biol. Chem. 265, 4064-4071, 1990			
A:Title: Affinity purification, peptide analysis, and cDNA sequence of the mouse interferon gamma receptor			
A:Reference number: A34568; MUID:90154093; PMID:2137461			
A:Accession: A34568			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-477 <COP>			
A:Cross-references: GB:J05265; NID:G197964; PIDN:AAA39178.1; PID:G309394			
J:Gray, P.W.; Leong, S.; Fennie, E.H.; Farrar, M.A.; Pingel, J.T.; Fernandez-Luna, J.; S. Proc. Natl. Acad. Sci. U.S.A. 86, 8497-8501, 1989			
A:Title: Cloning and expression of the cDNA for the murine interferon gamma receptor.			
A:Reference number: A34423; MUID:90046824; PMID:2530582			
A:Accession: A34423			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-94, 'E', '96-477 <GRA>			
A:Cross-references: GB:M26711; NID:G194126; PIDN:AAA37896.1; PID:G309330			
J:Hemi, S.; Peghini, P.; Metzler, M.; Marlin, G.; Dembic, Z.; Aguet, M. Proc. Natl. Acad. Sci. U.S.A. 86, 9901-9905, 1989			
A:Title: Cloning of murine interferon gamma receptor cDNA: expression in human cells mediated by a retrovirus			
A:Reference number: A34508; MUID:9009370; PMID:2532365			
A:Accession: A34508			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-94, 'E', '96-477 <HEM>			
A:Cross-references: GB:M28233; NID:G194131; PIDN:AAA37898.1; PID:G309331			
J:Munro, S.; Maniatis, T. Proc. Natl. Acad. Sci. U.S.A. 86, 9248-9252, 1989			
A:Title: Expression cloning of the murine interferon gamma receptor cDNA.			
A:Reference number: A36224; MUID:90083245; PMID:2531896			
A:Accession: A36224			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 10-477 <MUN>			
A:Cross-references: GB:M28995; NID:G194123; PIDN:AAA37895.1; PID:G309329			
J:Raval, P.; Oitic, S.; Russell, S.W.; Murphy, W.J. Gene 154, 219-223, 1995			
A:Title: Characterization of the 5' flanking region and gene encoding the mouse interferon gamma receptor			
A:Reference number: I48941; MUID:95197006; PMID:7890167			
A:Accession: I48941			

Job time : 21 secs

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2y 10 LLIILLSSATEIQPARVSLTPQKVRFO--SRNFHNLHWQAGSSLPNNNSIYFVQYKMYG 67
2b 16 VLMVVISLVFGISYDSDPYDDECTFKISLRNFRSILSWEL-----KNHSIVPTHYTLTY 70
2y 68 --QSQWED-KV--DCWGTALFCDLTNETLDPYELLYGRVMTACAGHSANTPTPTPW 122
2b 71 TIMSKPEDLVKVKNCANTTRSFCDLTDEWRSTHEAYV-TVLEGFSGNTTLFSCSHNFWLA 129
2y 123 WETKLDPPVVTITRVNASLRLVLRPPPELPNRQSGKNASMETYYGLVYRVFTINNSLEKE 182
2b 130 IDMSFEPPEPEIIVGFTNHINVVVKFPSI-----VEEELQFDLSLVIEEQSEGIVKK 180
2y 183 OKAYEGTORAVEIEG-----LPHSSYCVVAEMVQPMFDRSP-RSKERCVHI 229
2b 181 HKP-----EIKGNMSGNFTYIDKLIPNTNYCV--SVYLEHSDQAVIKSPKCTLL 230
2y 230 P 230
2b 231 P 231

RESULT 15
39073
Interferon alpha-beta receptor, beta subunit long form - human
1;Species: Homo sapiens (man)
2;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 01-Dec-2000
3;Accession: I39073; S59502
4;Domanski, P.; Witte, M.; Kellum, M.; Rubinstein, M.; Hackett, R.; Pitha, P.; Colamonic
J. Biol. Chem. 270, 21606-21611, 1995
5;Title: Cloning and expression of a long form of the beta subunit of the interferon alp
6;Reference number: I39073; MUID:95394915, PMID:7665574
7;Accession: I39073
8;Status: preliminary; translated from GB/EMBL/DBJ
9;Molecule type: mRNA
10;Residues: 1-515 <RES>
11;Cross-references: EMBL:U29584; NID:9993040; PIDN:AA050202.1; PID:9993041
12;Lutfalla, G.; Holland, S.J.; Cinato, E.; Monneron, D.; Reboul, J.; Rogers, N.C.; Smith
EMBO J. 14, 5100-5108, 1995
13;Title: Mutant USA cells are complemented by an interferon-alpha-beta receptor subunit
14;Reference number: S59501; MUID:96067138; PMID:7588638
15;Accession: S59502
16;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
17;Residues: 1-150, 'M', 152-515 <LUT>
18;Cross-references: GB:L41942; NID:9995292; PIDN:AA046413.1; PID:9995293
19;Keywords: alternative splicing; cytokine receptor

Query Match 9.9%; Score 122.5; DB 2; Length 515;
Best Local Similarity 23.7%; Pred. No. 0.00087;
Matches 57; Conservative 42; Mismatches 97; Indels 45; Gaps 11;

QY 10 LLIILLSSATEIQPARVSLTPQKVRFO--SRNFHNLHWQAGSSLPNNNSIYFVQYKMYG 67
Db 16 VLMVVISLVFGISYDSDPYDDECTFKISLRNFRSILSWEL-----KNHSIVPTHYTLTY 70
QY 68 --QSQWED-KV--DCWGTALFCDLTNETLDPYELLYGRVMTACAGHSANTPTPTPW 122
Db 71 TIMSKPEDLVKVKNCANTTRSFCDLTDEWRSTHEAYV-TVLEGFSGNTTLFSCSHNFWLA 129
QY 123 WETKLDPPVVTITRVNASLRLVLRPPPELPNRQSGKNASMETYYGLVYRVFTINNSLEKE 182
Db 130 IDMSFEPPEPEIIVGFTNHINVVVKFPSI-----VEEELQFDLSLVIEEQSEGIVKK 180
QY 183 OKAYEGTORAVEIEG-----LPHSSYCVVAEMVQPMFDRSP-RSKERCVHI 229
Db 181 HKP-----EIKGNMSGNFTYIDKLIPNTNYCV--SVYLEHSDQAVIKSPKCTLL 230
QY 230 P 230
Db 231 P 231
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Search completed: March 12, 2004, 16:00:07

Db 5 LLPFLVITSSLSLEFIAYGTLPSPSYWFEARFQHLHWK---PIPNQSESTYFEVAL 61
QY 64 KMYGOSQWEDKVDGTTALFCDLTNETLDPVELYVG---RVMTACAGRHSAWTRT-PRF 119
Db 62 KOYGNSTWHDHICRKAQALSCLDTFTFLDYHRSYGYRVARVDNSQYSNWTTTETRF 121
QY 120 TPWWTETKDPVVTITRNVASLVL-----LRPELPNRSQGNKSMETTYGLVY-- 170
Db 122 T-----VDEVLTVDSV--TLKAMDGIYGTIHPPR-PTITPAGDE-----YEQFKD 166
QY 171 -RVFTINNSLEKEQKAYEGTORAVE-----IEGLPHSSYCVVAEYQMFRRGRPR---S 222
Db 167 LAVYKI--SIRFESLKNATKVKQETTLTVPVGRKFCV---KVLPRLESRLINKAENS 221
QY 223 KERCVHI 229
Db 222 ERQCLLI 228

RESULT 2
ID IL10R HUMAN STANDARD; PRT; 578 AA.
AC Q13651;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-10 receptor alpha chain precursor (IL-10R-A) (IL-10R1).
GN IL10RA OR IL10R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoma;
RX MEDLINE=94165477; PubMed=8120391;
RA Liu Y., Wei S.H.-Y., Ho A.S.-Y., de Waal Malefyt R., Moore K.W.;
RT "Expression cloning and characterization of a human IL-10 receptor.";
RL J. Immunol. 152:1821-1829(1994).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS VAL-61; ILE-113; GLY-159; GLN-212;
RP ARG-351 AND LEU-420.
RA Rieder M.J., Hastings N.C., Arnel T.Z., Carrington D.P., Ozuna M.,
RA Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for IL-10; binds IL-10 with a high affinity.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Spleen, thymus, and PBMC. Weak expression in
pancreas, skeletal muscle, brain, heart, and kidney. Placenta,

CC lung, and liver showed intermediate levels. Monocytes, B cells,
CC large granular lymphocytes, and T cells express high levels.
CC -!- SIMILARITY: Belongs to the type II cytokine family of receptors.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U00672; AAA17896.1; -;
CC EMBL: AV195619; AAN86349.1; -;
CC EMBL: BC028082; AAN82082.1; -;
CC PIR: I56215; I56215.
CC PDB: 1J7V; 19-SEP-01.
CC PDB: 1LQ5; 17-JUL-02.
CC Genew; HGNC:5964; IL10RA.
CC MIM: 146933; -;
CC GO: GO:0005886; C:plasma membrane; TAS.
CC GO: GO:0004920; F:interleukin-10 receptor activity; TAS.
CC GO: GO:0004872; F:receptor activity; TAS.
CC InterPro; IPR000282; Cytok_receptor_2.
CC Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;
CC 3D-structure.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 578 INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.
FT DOMAIN 22 235 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 257 578 CYTOPLASMIC (POTENTIAL).
FT DISULFID 202 223 POTENTIAL.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 61 61 L -> V. /FTID=VAR_016294.
FT VARIANT 113 113 V -> I. /FTID=VAR_016295.
FT VARIANT 159 159 S -> G. /FTID=VAR_016296.
FT VARIANT 212 212 R -> Q. /FTID=VAR_016297.
FT VARIANT 351 351 G -> R. /FTID=VAR_016298.
FT VARIANT 420 420 S -> L. /FTID=VAR_016299.
FT SEQUENCE 578 AA; 62903 MW; EE1B29064338157C CRC64;
SQ
Query Match 14.0%; Score 174.5; DB 1; Length 578;
Best Local Similarity 28.7%; Pred. No. 8e-09;
Matches 72; Conservative 37; Mismatches 95; Indels 47; Gaps 15;
QY 1 MPPGHCLGLLIILLS-----SATEIQARVSLTPQKVFQSRNFHILHWQAGSSLP 53
Db 1 MLP--CLVVLLAALLSLRGLSDAHTLP-----SPPSWFEAEFFHILHW---TPIP 49
QY 54 --SNNSYFVQYKMGQSQWEDKVDGTTALFCDLTNETLDPVELY--YGRVMTACGR 109
Db 50 NQSESTCYEVALRYGIESNWSISNC--SQTLSDYDLTAVTLDLHNGYRVARVADGSR 107
QY 110 HSAWTRT-PRFTPWETKLPDPVVTITRNVASLR--VLLRPPELPNRSQGNKSMETTY 166
Db 108 HSNVTVNTAFS-----VDEVLTGVSVNLEHTNGFGLKGLPRPKMAPANDTYESIF 161
QY 167 GLVYRVFTTINNSLEKEQKAYEGTORAVEIEGLPHSS-----YCVVAEYQMFRRGRSPR 221
Db 162 S-HPREVEI--AIRKVPQNETFTTHKKVKHENFSLTSGEVGEFCV---QVKPSVASRSNK 215
QY 222 ---SKERCVHI 229

Query Match 13.9%; Score 173; DB 1; Length 349;
Best Local Similarity 27.8%; Pred. No. 6e-09;

15-JUL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Interferon-alpha/beta receptor beta chain precursor (IFN-alpha-REC)
(Type I interferon receptor) (IFN-R) (Interferon alpha/beta receptor-
2).
DN IFNAR2 OR IFNAR3.
DS Ovis aries (Sheep).
DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
DC Bovidae; Caprinae; Ovis.
DX NCBI_TaxID=9940;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Endometrium;
RX MEDLINE=98006426; PubMed=9349203;
RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
RT "Molecular cloning of ovine and bovine type I interferon receptor
subunits from uteri, and endometrial expression of messenger
ribonucleic acid for ovine receptors during the estrous cycle and
pregnancy";
RL Endocrinology 138:4757-4767(1997).
CC -!- FUNCTION: Receptor for interferons alpha and beta. Probably
involved in signal transduction by interacting with the tyrosine
kinase, JAK1.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in all tissues examined except
conceptus at day 15 of pregnancy.
CC -!- SIMILARITY: Belongs to the type II cytokine family of receptors.
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CC EMBL; U65979; AB84232.1; -
CC InterPro; IPR000282; Cytok_receptor_2.
CC InterPro; IPR008957; FN.III-like.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 536
FT DOMAIN 27 246
FT TRANSMEM 247 267
FT DOMAIN 268 536
FT DOMAIN 358 372
FT REPEAT 358 362
FT REPEAT 363 367
FT REPEAT 368 372
FT DISULFID 85 93
FT CYSLOOP 210 230
FT CARBOHYD 58 58
FT CARBOHYD 87 87
FT CARBOHYD 101 101
FT CARBOHYD 147 147
FT CARBOHYD 191 191
FT CARBOHYD 536 536
FT SEQUENCE 536 AA; 60260 MW; 1055F27D80945150 CRC64;
Query Match 12.6%; Score 156; DB 1; Length 536;
Best Local Similarity 26.9%; Pred. No. 4.2e-07;
Matches 58; Conservative 39; Mismatches 73; Indels 46; Gaps 12;
QY 32 KVRQSRPHILHWQAGSSLPNNISLVFVCKMVG--QSQWED-KV--DCWGTALFCD 86
DB 42 KMRP--RNFQSLSWEL-----KRSIVFTHYTWYIMSPKDMVKVCKINIRSFCD 94
QY 87 LTNETLDPVLYYGR-----VMTACAGRHSAWTRTPPTPWETKLDP--VVVIT 135
DB 95 LTDVWNRDWMVISQVGVYRENAVWVSCMGSFELASDKP-----LDPPKEIVDFT 145
QY 136 -RVNASLVLRLPPLPRLPNRNSGKKNASMETYGLVYRVFTINNSLEKEQKAYGT---QR 191

146 NNISVWFRDSDRIPSEELQFLAIEEHAG-----NSVKHQPOITGNITENP 196
QY 192 AVEIEGLPHSSYCVVAEMVQPMFDRSPRSKRCV 227
DB 197 NYVIDKLIPNTNYC-ISVPEEPKPRKINRSLPKCI 231
RESULT 6
TF_CAVPO
ID TF_CAVPO STANDARD; PRT; 289 AA.
AC Q9JLUS;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tissue factor precursor (TF) (Coagulation factor III).
GN F3.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RX MEDLINE=20206020; PubMed=10744153;
RA Shi R.J., Li W.Z., Marder V.J., Sporn L.A.;
RT "Cloning of guinea pig tissue factor cDNA: comparison of primary
structure among six mammalian species";
RL Thromb. Haemost. 83:455-461(2000).
CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CIRCULATING FACTOR VII OR VIIA. THE [TF.VIIA] COMPLEX ACTIVATES
FACTORS IX OR X BY SPECIFIC LIMITED PROLYSIS. TF PLAYS A ROLE IN
NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the tissue factor family.
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or send an email to license@isb-sib.ch).
CC EMBL; AF131949; AAF36523.1; -
CC HSP; P13726; ITFH.
CC InterPro; IPR000282; Cytok_receptor_2.
CC InterPro; IPR008957; FN.III-like.
CC InterPro; IPR001187; Tissue factor.
CC Pfam; PF01108; Tissue fac; I.
CC PRINTS; PR00346; TISSUEFACTOR.
CC PROSITE; PS00621; TISSUE_FACTOR; FALSE_NEG.
KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
FT SIGNAL 1 32
FT CHAIN 33 289
FT DOMAIN 33 247
FT TRANSMEM 248 268
FT DOMAIN 269 289
FT SITE 44 46
FT SITE 75 77
FT CARBOHYD 41 41
FT CARBOHYD 111 111
FT CARBOHYD 151 151
FT CARBOHYD 164 164
FT DISULFID 79 87
FT DISULFID 213 236
FT LIPID 271 271
FT SEQUENCE 289 AA; 32456 MW; 7AB97F8F58199FBI CRC64;
Query Match 12.4%; Score 154; DB 1; Length 289;
Best Local Similarity 25.4%; Pred. No. 3e-07;


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Matches 60; Conservative 45; Mismatches 101; Indels 30; Gaps 13;
QY 7 LGLLIILLSSATETQPARVSLTPQKVFQGRNFHNLHWAGSSLPNSNIYVQVQMY 66
DB 21 LLGWLVQVAGAEGL-----PVKPNLTWKSTNFKTLEWE-----PKPINN-VYTVQI--- 68
QY 67 GOSQWED-KVDCWGTTALFCDLTNETL-DPVELYXGRVMTACAG-----RHSAWTRTPRF 119
DB 69 -STALEDNKSIKFSITATECDLTSETMAENVQOTYLARVISLLPSTGFLSDAVYSNSPEF 127
QY 120 TPWETKL-DPPVVTITRNASLRVLLPPELPNRSQGNASMETIYG--LVTRVFTIN 176
DB 128 TPYQETNLGQPKIESFKLVGTGLANTVTRDTQTLARS-NGTFLSLDFGKNLQVLYWYR 186
QY 177 NLEKEQKAYEQTOR-AVEIEGLPHSSYCVVAEWYQP--NFDPRSRSKERCYVHI 229
DB 187 SSTTGKKTANTWNEFLIDVD---KQDQCFPVQAVIPSRDKNSPSITVCIHL 239
RESULT 7
ID T10S HUMAN STANDARD; PRT; 325 AA.
AC Q08334;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
DE (Cytokine receptor class-II CRF2-4).
GN IL10RB OR CRFB4
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
CX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Petal brain;
RX MEDLINE=93300510; PubMed=8314576;
RA Lutfalla G, Gardiner K, Uze G;
RT "A new member of the cytokine receptor gene family maps on chromosome
RT 21 at less than 35 kb from IFN2A";
RL Genomics 16:366-373(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96054036; PubMed=7563119;
RA Lutfalla G, McInnis M.G., Antonarakis S.E., Uze G;
RT "Structure of the human CRFB4 gene: comparison with its IFNAR
RT neighbor.";
RL J. Mol. Evol. 41:338-344(1995).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=97459974; PubMed=9312047;
RA Korten S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu W.,
RA Pestka S.;
RT "Identification and functional characterization of a second chain of
RT the interleukin-10 receptor complex.";
RL EMBO J. 16:5894-5903(1997).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=10875937;
RA Xie M.-H., Agarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J.,
RA Wood W.I., Goddard A.D., Gurney A.L.;
RT "Interleukin (IL)-22, a novel human cytokine that signals through the
RT interferon receptor-related proteins CRF2-4 and IL-22R.";
RL J. Biol. Chem. 275:31335-31339(2000).
CC -1- FUNCTION: Receptor for IL10 and IL22. Serves as an accessory chain
CC essential for the active IL10 receptor complex and to initiate
CC IL10-induced signal transduction events.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the type II cytokine family of receptors.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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CC -----
DB EMBL; Z17227; CAA78933.1; -
DB EMBL; U08988; AAA86872.1; -
DB PIR; A47003; A47003.
DB HSP; P13726; ITHF.
DB Genew; HGNC:5965; IL10RB.
DB MM; 123889; -
DB GO; GO:0016021; C:integral to membrane; TAS.
DB GO; GO:0005886; C:plasma membrane; TAS.
DB GO; GO:0004920; F:interleukin-10 receptor activity; TAS.
DB GO; GO:0004872; F:receptor activity; TAS.
DB GO; GO:0006955; P:immune response; TAS.
DB GO; GO:0006954; P:inflammatory response; TAS.
DB GO; GO:0007165; P:signal transduction; TAS.
DB InterPro; IPR000282; Cytok_receptor_2.
DB InterPro; IPR008957; FN_III-like.
DB InterPro; IPR003961; FN_III.
DB InterPro; IPR001187; Tissue_factor.
DB Pfam; PF01108; Tissue_fac; I.
DB SMART; SM00060; FN3; 2.
DB Receptor; Transmembrane; Glycoprotein; Signal.
KW SIGNAL
FT CHAIN 1 19
FT DOMAIN 20 325
FT TRANSMEM 221 242
FT TRANSMEM 243 325
FT DOMAIN 113 205
FT DISULFID 66 74
FT DISULFID 188 209
FT CARBOHYD 49 49
FT CARBOHYD 68 68
FT CARBOHYD 102 102
FT CARBOHYD 161 161
FT CONFLICT 124 124
FT CONFLICT 269 273
FT CONFLICT 274 325
FT CONFLICT 325 AA; 37011 MW; 66706C79F814B23 CRC64;
SQ
Query Match 12.3%; Score 153; DB 1; Length 325;
Best Local Similarity 27.2%; Pred. No. 4.3e-07;
Matches 61; Conservative 29; Mismatches 96; Indels 38; Gaps 10;
QY 14 LLSATETIQPARVSLTPQKVFQGRNFHNLHWAGSSLPNSNIYVQVQMYGQSOWED 73
DB 13 LLVSALGMVP-----PPENVNMSVNFKNILQWES-PAPAKGNLTFTAQVLSY--RIFQD 64
QY 74 KVDGCGTTALFCDLTNETLDPYELYXGRVMTACAGRHSAMTRTPRTPPWETKLDPPVVT 133
DB 65 K-CWNTLTETCDFS--SLSKYGDHILRVRAEFADEHSDWNI--TFQVDDTIIGPFQM 119
QY 134 ITRVNASLRVLLRPPELPNRSQSG--KNASMETIYGIVYVFTINNSLEKEQKAYEQTOR 191
DB 120 VEVLADSLHMRFLAPKIENEYETWTKN-----VNSWTNVQVWK-----NGTDE 165
QY 192 AVEI-----EGLPHSSYCVVAEWYQPMFDRSPRSKERC 226
DB 166 KFOITPQYDFEVLNLEWYTCVQVRGFLPDRNKAGEWSEPC 209
RESULT 8
ID TF_BOVIN STANDARD; PRT; 292 AA.
AC P30931;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tissue factor precursor (TF) (Coagulation factor III).
GN F3.
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OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP TISSUE=Adrenal gland;
RX MEDLINE=92109720; PubMed=1764065;
RA Takayoshi Y., Muta T., Miyata T., Iwanaga S.;
RT "cDNA and amino acid sequences of bovine tissue factor.";
RL Biochem. Biophys. Res. Commun. 181:1145-1150(1991).
CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC CIRCULATING FACTOR VII OR VITA. THE [TF:VIA] COMPLEX ACTIVATES
CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the tissue factor family.
CC
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CC
CC EMBL; S74147; AAB20755.1; ..
DR PIR: JQ1319; KFB03.
DR HSSP: P24055; 1A21.
DR InterPro: IPR000282; Cytok receptor 2.
DR InterPro: IPR009557; FN11-like.
DR Pfam: PF01108; Tissue factor.
DR PRINTS: PRO0346; TISSUEFACTOR.
DR PROSITE: PS00621; TISSUE FACTOR; 1.
KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW Palmitate.
FT SIGNAL 1 35
FT CHAIN 36 292 TISSUE FACTOR.
FT DOMAIN 36 248 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 249 271 POTENTIAL.
FT DOMAIN 272 292 CYTOPLASMIC (POTENTIAL).
FT SITE 46 48 WKS MOTIF.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 81 89 BY SIMILARITY.
FT DISULFID 215 238 BY SIMILARITY.
FT LIPID 274 274 S-palmitoyl cysteine (By similarity).
SQ SEQUENCE 292 AA; 32475 MW; 5E471D92BFBC163 CRC64;
Query Match 12.1%; Score 150; DB 1; Length 292;
Best Local Similarity 24.9%; Pred. No. 7.3e-07;
Matches 60; Conservative 47; Mismatches 90; Indels 44; Gaps 13;
7 LGLGLIIL---LSSATEIOPARVSTPKVQFOSRNFHILHWQAGSLPNNISYFVQY 63
21 LFGVLVIQAGVAGTVDV-----VVAINITKSNFKTILEWSP---KXINHYVTVQI 70
64 KMYGQSQWEDKVDGNGTTFALFCDLTNETL-DPYELLYGRVMTACAGHSA-----WTRTP 117
71 SP-RLGNWKNK--CFYTTNTECDVTDVETKRVRETYLARVLSPADTSSSTVEPPFTNSP 127
118 RFTPWETKLDPPVVTI-----TRVNASL---RVLLRPPE--LPNNQSGKNVSMETVYG 167
128 EFTPLENLNGQFTTQSEFQVGTCLNVTVQARTLVTRANSALSLRDVFGKDLNLTLYW 187
168 LVYRVFTINNSLEKQKAYEGTQRAVEIGLPHSSYC--VVAENYQPMFDRRSPRSKER 225
188 KA-----SSGKKKATNTNTNGFLIDVD---KGENYCFHVQAVILSRVNVCKSPSPDIK 237

QY 226 C 226
DB 238 C 238
RESULT 9
TF HUMAN
ID TF HUMAN STANDARD; PRT; 295 AA.
AC P13726;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tissue factor precursor (TF) (Coagulation factor III)
DE (Thromboplastin) (CD142 antigen).
GN F3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=89247359; PubMed=2719931;
RX Mackman N., Morrissey J.H., Fowler B., Edgington T.S.;
RT "Complete sequence of the human tissue factor gene, a highly
RT regulated cellular receptor that initiates the coagulation protease
RT cascade.";
RL Biochemistry 28:1755-1762(1989).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=87260946; PubMed=3037536;
RX Spicer E.K., Horton R., Bloem L., Bach R., Williams K.R., Guha A.,
RA Kraus J., Lin T.C., Nemerson Y., Konigsberg W.H.;
RT "Isolation of cDNA clones coding for human tissue factor: primary
RT structure of the protein and cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5148-5152(1987).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=87244317; PubMed=3297348;
RA Morrissey J.H., Fakhrai H., Edgington T.S.;
RT "Molecular cloning of the cDNA for tissue factor, the cellular
RT receptor for the initiation of the coagulation protease cascade.";
RL Cell 50:129-135(1987).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=8050796; PubMed=2823875;
RA Scarpati E.M., Wen D., Broze G.J. Jr., Milewich J.P.,
RA Flendermeyer R.R., Siegel N.R., Sadler J.E.;
RT "Human tissue factor: cDNA sequence and chromosome localization of
RT the gene.";
RL Biochemistry 26:5234-5238(1987).
RN [5]
RN SEQUENCE FROM N.A.
RX MEDLINE=88100453; PubMed=3424286;
RA Fisher K.L., Gorman C.M., Vehar G.A., O'Brien D.P., Lawn R.M.;
RT "Cloning and expression of human tissue factor cDNA.";
RL Thromb. Res. 48:89-99(1987).
RN [6]
RN SEQUENCE FROM N.A., AND VARIANTS ALA-36 AND VAL-145.
RA Rieder M.J., Amel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth S.J., Yi C., Nickerson D.A.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RN SEQUENCE FROM N.A.
RA Collier R.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [8]
RN SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Ioshizuka S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RN [10]
RN [11]
RN [12]
RN [13]
RX MEDLINE=96175641; PubMed=8598903;
RX MEDLINE=96190957; PubMed=8609606;
RX Muller Y.A., Ullsch M.H., de Vos A.M.;
RT "The crystal structure of the extracellular domain of human tissue
RT factor refined to 1.7-A resolution.";
RL J. Mol. Biol. 256:144-159(1996).
RX X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 33-243.
RX MEDLINE=96175641; PubMed=8598903;
RX Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor
RT VIIa with soluble tissue factor.";
RL Nature 380:41-46(1996).
RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 37-242 IN COMPLEX WITH FVIIA.
RX MEDLINE=99126538; PubMed=9945787;
RX Zhang E., St Charles R., Tulinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa
RT inhibited with a BPTI mutant.";
RL J. Mol. Biol. 285:2089-2104(1999).
CC -|- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC CIRCULATING FACTOR VII OR VIIA. THE [TF-VIIA] COMPLEX ACTIVATES
CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- INDUCTION: TF EXPRESSION IS HIGHLY DEPENDENT UPON CELL TYPE. TF
CC CAN ALSO BE INDUCED BY THE INFLAMMATORY MEDIATORS INTERLEUKIN 1
CC AND TNF, AS WELL AS BY ENDOTOXIN, TO APPEAR ON MONOCYTES AND
CC VASCULAR ENDOTHELIAL CELLS AS A COMPONENT OF CELLULAR IMMUNE
CC RESPONSE.
CC -|- SIMILARITY: Belongs to the tissue factor family.
CC -|- DATABASE: NMR-PRO; NMR-CD guide CD142 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd142.htm".
CC -----
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CC -----
CC ENBL; J02931; AAA61150.1; -
CC ENBL; J02845; AAA61151.1; -
CC ENBL; J02846; AAA61152.1; -
CC ENBL; M27436; AAA36734.1; -
CC ENBL; A19048; CAA01438.1; -
CC ENBL; AF540377; AAN01236.1; -
CC ENBL; AL138758; CAC15961.1; -
CC ENBL; BC011029; AAH11029.1; -
CC FIR; A43645; KFHJ3.
CC PDB; 1BOY; 10-JUN-96.
CC PDB; 2HFT; 29-JAN-96.
CC PDB; 1DAN; 04-SEP-97.
CC PDB; 1AHW; 19-AUG-98.
CC PDB; 1TPH; 19-AUG-98.
CC PDB; 1FAK; 03-DEC-99.
CC PDB; 1JPS; 18-DEC-02.
CC Genew; HGNC:3541; P3.
CC MIM; 134390; -
CC GO; GO:0016021; C: integral to membrane; TAS.
CC GO; GO:0003801; F: blood coagulation factor activity; TAS.
CC InterPro; IPR000282; Cytok_receptor_2.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR001187; Tissue factor.
CC Pfam; PF01108; Tissue fac; I.
CC PRINTS; PR00346; TISSUEFACTOR.
CC PROSITE; PS00621; TISSUE_FACTOR; 1.
CC Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW Palmitate; 3D-structure; Polymorphism.
FT SIGNAL 1 32
FT CHAIN 33 295 TISSUE FACTOR.
FT DOMAIN 33 251 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 252 274 POTENTIAL.
FT DOMAIN 275 295 CYTOPLASMIC (POTENTIAL).
FT SITE 46 48 WKS MOTIF.
FT SITE 77 79 WKS MOTIF.
FT SITE 190 192 WKS MOTIF.
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 81 89
FT DISULFID 218 241
FT LIPID 277 277
FT VARIANT 36 36 S-palmitoyl cysteine.
FT VARIANT 145 145 T -> A.
FT VARIANT 163 163 I -> V.
FT VARIANT 163 163 /FTID=VAR_014299.
FT VARIANT 260 260 R -> W (in dbSNP:5901).
FT CONFLICT 42 49 /FTID=VAR_012008.
FT STRAND 50 51 V -> A (IN REF. 4).
FT TURN 52 58
FT STRAND 64 72
FT TURN 73 74
FT STRAND 78 84
FT STRAND 88 90
FT STRAND 92 95
FT HELIX 96 98
FT TURN 99 100
FT STRAND 103 111
Query Match 11.7%; Score 145.5; DB 1; Length 295;
Best Local Similarity 26.1%; Pred. No. 2e-06;
Matches 61; Conservative 38; Mismatches 90; Indels 45; Gaps 14;
QY 16 SSATEIQARVSLFPQKRFQSRNFHILWQAGSSLPSSNNISYFVQYKMGQSQWEDKV 75
DB 32 ASGITNTVAAYNLT-----WKSTNFKTILEWEP-----KPVNQVYTVQIST-KSGDWKSK- 80
QY 76 DCGTTTALFCDLTNETL-DPVELYGVGMVACAGR-----HSAWTRTPRTFPMWETK 126
DB 81 -CFYTTDTECDLTDDEIVKDVQKTVLRFVSPAGNVSTGAGEPLYSFPTPILETN 139

QY 127 LDPVWTVI-----TRVNASL---RVLLRPPELPNRNOSGNKSNMTEYVG--LVVRVFTIN 176
Db 140 LGQTFIQSFEQVGRKYNVVEDETLVR-----RNNT--FLSLRDVFGKDLITYYWK 191
QY 177 NSLKEKQAYEGTOR-AVEIEGLPHSYCYVVAEMYP--MFDRSRSPKERCVCV 227
Db 192 SSSGKKTKAKTNTNEFLIDVD---KGENYCFVSQVAVIPSRVTNRKSTDSPEVCM 242

RESULT 10
TF_RABIT
ID TF_RABIT STANDARD; PRT; 292 AA.
AC P24055;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tissue factor precursor (TF) (Coagulation factor III).
FN 3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_taxID=9986;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=91200676; PubMed=1840552;
RA Andrews B.S., Rehmtulla A., Fowler B.J., Edgington T.S., Mackman N.;
RT "Conservation of tissue factor primary sequence among three mammalian
RT species.";
RL Gene 98:265-269(1991).
RN [2]
RN SEQUENCE OF 33-292 FROM N.A.
RP STRAIN=New Zealand white; TISSUE=Brain;
RX MEDLINE=92081032; PubMed=1746002;
RA Pawashe A., Ezekowitz M., Lin T.C., Horton R., Bach R., Konigsberg W.;
RT "Molecular cloning, characterization and expression of cDNA for
RT rabbit brain tissue factor.";
RL Thromb. Haemost. 66:315-320(1991).
RN [3]
RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 36-240.
RX MEDLINE=98266351; PubMed=9605315;
RA Muller Y.A., Kelley R.F., de Vos A.M.;
RT "Hinge bending within the cytokine receptor superfamily revealed by
RT the 2.4 A crystal structure of the extracellular domain of rabbit
RT tissue factor.";
RL Protein Sci. 7:1106-1115(1998).
CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
CC FACTORS IX OR X BY SPECIFIC LIMITED PROLYSIS. TF PLAYS A ROLE IN
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: BRAIN, HEART.
CC -!- SIMILARITY: Belongs to the tissue factor family.
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CC
CC EMBL; M55390; AAA63469.1; -
CC EMBL; X53521; CAA37597.1; -
CC FIC; JU0441; KFRB3.
CC PDB; 1A21; 27-MAY-98.
CC InterPro; IPR000282; Cytok_receptor_2.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR001187; Tissue_factor.
CC Pfam; PF01108; Tissue_fac; 1.
CC PRINTS; PR00346; TISSUEFACTOR.

DR PROSITE; PS00621; TISSUE FACTOR; 1.
KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW Palmitate; 3D-structure.
FT SIGNAL 1 32
FT CHAIN 33 292
FT DOMAIN 251 271
FT TRANSMEM 272 292
FT SITE 44 46
FT SITE 75 77
FT CARBOHYD 41 41
FT CARBOHYD 114 114
FT CARBOHYD 154 154
FT CARBOHYD 167 167
FT CARBOHYD 182 182
FT DISULFID 79 87
FT DISULFID 216 239
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FT STRAND 62 69
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FT HELIX 90 93
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FT TURN 211 212
FT STRAND 216 222
FT TURN 224 225
FT STRAND 231 231
FT STRAND 238 239
SQ SEQUENCE 292 AA; 32738 MW; 4860A1CADBACCF71 CRC64;

Query Match 11.8; Score 144.5; DB 1; Length 292;
Best Local Similarity 24.8; Pred. No. 2.4e-06;
Matches 61; Conservative 43; Mismatches 99; Indels 43; Gaps 13;

QY 2 MPKHCLLLILLSSATEIQPARVSLTPQKVRFSQSRNFHILHWQAGSSLPNNNSIYFV 61
Db 16 VPYVLLGNLLAQVAAADTGTAYNLT-----WKSTNFKTILEWEP---KSIDHVVTV 66
QY 62 QYKMYGOSQHEKVDGCTGTALPCDLTNETL-DPYELYGRVMTACAGHSA----- 112
Db 67 QISTRLN-WKSK--CFLTAETECDLTDEVKDVGTVMARVLSYPARNGTTFGPPEPP 123
QY 113 WTRTERTPWETKLDPPVY-TITRVNASLRVLRRPE-LPNRNQ-----GKNASM 162
Db 124 FRNSPFTPLDNLGQPIQSFEQVGTKLNVQDARTLVRNGTFLSLRAVFGKDLNY 183
QY 163 ETYVGLVYRVFTINNSLEKEQKAYEGTORAVEIEGLPHSSYCYVVAEMYPQMPDR--RSP 220
Db 184 TLYY---WRA-----SSTGKKTATTNTNEFLIDVD---KGENYCFVSQVAVIPSRKQRSP 233
QY 221 RSKERC 226
Db 234 ESLTEC 239

Db	68	DEAKWLKVP	ECQHTTTTKCFE	LLDTNVIKQFVRABEGNSTSWNEVDFFI	PFYTAH 12
Qy	127	LDPPVVTIT	RVNASLVRLLR	PPPELNRNOSGKNVSM	E-TYGLVYRVFTNNLSKEQKA 185
Db	128	MSPPEVRLE	AEADKAILVHSPP	-----GQDGNWALEKPSF	SYTIRIMQKSSS---DKKT 179
Qy	186	YEGTQRAVE	IEGLIPHSYCVV	VAEMQPMFDRRS	PRSKERCVCV 227
Db	180	INSTYYVEK	IPPELLPTT	YCLVKAHPSLKHSN	YSTVQCI 221
<p>RESULT 12</p> <p>INGR MOUSE</p> <p>ID INGR MOUSE STANDARD; PRT; 477 AA.</p> <p>AC P15261;</p> <p>DT 01-APR-1990 (Rel. 14, Created)</p> <p>DT 01-AUG-1990 (Rel. 15, Last sequence update)</p> <p>DT 15-MAR-2004 (Rel. 43, Last annotation update)</p> <p>DE Interferon-gamma receptor alpha chain precursor.</p> <p>GN IFNGR1 OR IFNGR.</p> <p>OS Mus musculus (Mouse).</p> <p>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p> <p>OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.</p> <p>OX NCBI_TaxID=10090;</p> <p>RN SEQUENCE FROM N.A.</p> <p>RP MEDLINE=90083245; PubMed=2531896;</p> <p>RA Munro S., Maniatis T.;</p> <p>RT "Expression cloning of the murine interferon gamma receptor cDNA.";</p> <p>RL Proc. Natl. Acad. Sci. U.S.A. 86:9248-9252(1989).</p> <p>RN SEQUENCE FROM N.A.</p> <p>RP MEDLINE=90046824; PubMed=2530582;</p> <p>RA Gray P.W., Jeong S., Fennie E.H., Farrar M.A., Pingel J.T.,</p> <p>RA Fernandez-Luna J., Schreiber R.D.,</p> <p>RT "Cloning and expression of the cDNA for the murine interferon gamma</p> <p>RT receptor.";</p> <p>RL Proc. Natl. Acad. Sci. U.S.A. 86:8497-8501(1989).</p> <p>RN SEQUENCE FROM N.A.</p> <p>RP MEDLINE=90093170; PubMed=2532365;</p> <p>RA Hemmi S., Peghini P., Metzler M., Merlin G., Dembic Z., Aguet M.;</p> <p>RT "Cloning of murine interferon gamma receptor cDNA: expression in</p> <p>RT human cells mediates high-affinity binding but is not sufficient to</p> <p>RT confer sensitivity to murine interferon gamma.";</p> <p>RL Proc. Natl. Acad. Sci. U.S.A. 86:9901-9905(1989).</p> <p>RN SEQUENCE FROM N.A.</p> <p>RP MEDLINE=90036866; PubMed=2530216;</p> <p>RA Kumar C.S., Muthukumaran G., Frost L.J., Noe M., Ahn Y.H.,</p> <p>RA Mariano T.M., Pestka S.;</p> <p>RT "Molecular characterization of the murine interferon gamma receptor</p> <p>RT cDNA.";</p> <p>RL J. Biol. Chem. 264:17939-17946(1989).</p> <p>RN SEQUENCE FROM N.A.</p> <p>RP MEDLINE=90154099; PubMed=2137461;</p> <p>RA Cofano F., Moore S.K., Tanaka S., Yuhki N., Landolfo S.,</p> <p>RA Appella E.;</p> <p>RT "Affinity purification, peptide analysis, and cDNA sequence of the</p> <p>RT mouse interferon gamma receptor.";</p> <p>RL J. Biol. Chem. 265:4064-4071(1990).</p> <p>RN SEQUENCE OF 1-28 FROM N.A.</p> <p>RP MEDLINE=95197006; PubMed=7890167;</p> <p>RA Raval P., Obici S., Russell S.W., Murphy W.J.;</p> <p>RT "Characterization of the 5' flanking region and gene encoding the</p> <p>RT mouse interferon-gamma receptor.";</p> <p>RL Gene 134:219-223(1995).</p> <p>CC -!- FUNCTION: Receptor for interferon gamma. Two receptors bind one</p> <p>CC -!- INTERFERON gamma dimer.</p> <p>CC -!- SUBCELLULAR LOCATION: Type I membrane protein.</p> <p>CC -!- PTM: Phosphorylated at Ser/Thr residues.</p>					

QY 8 LGLILLSSATEIQPARVSLTPQKVRFSORNFHILHWQAGSSLPNSNYSFYQKMYG 67
 DB 18 LCCLLQVAGIAGEKARNLT-----WISDFKILEWQP-----KPNYYTYVQISDES 68
 QY 69 QSQWEDKVDWCWTTALFCDLITNETL-DPYELYIGRWMT-----ACAGRHS 112
 DB 69 RN-WKNK--CFSTDTTECDLTDEIVKDVMTWAEAKVLSVPRNSVHGQDGLVHGEPP 125
 QY 113 WRTPTFTPWETKLDPPV-----TITRVNASLRVLLRPPPLPNRN 154
 DB 126 FTAFAKFLPYRTNLGQPIVQIQFQDGRKLVVVKDSLTVKNGTFTLT-----RQ 177
 QY 155 QSGKASMETYGLVYRVFTTNNLSLEKQAYEGTQRAVEIGLPHSSYC--VVAENYQ 212
 DB 178 VFGKDLG----YIIIVRK---GSSTGKNTINTNEFSIDVEEGV---SYCFFVQAMIFS 227
 QY 213 PMFDRSRPSKERC 226
 DB 228 RKTQNSQSGSSTVC 241

RESULT 14

INR1_BOVIN STANDARD; PRT; 560 AA.
 ID INR1_BOVIN
 AC Q04730;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).
 GN IFNAR1 OR IFNAR.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP MEDLINE=93076908; PubMed=1446745;
 RA Mouchel-Vielh E, Lufalla G, Mogensen K.E., Uze G;
 RT "Specific antiviral activities of the human alpha interferons are
 RL determined at the level of receptor (IFNAR) structure."
 RL FEBS Lett. 313:255-259(1992).
 RN [2]
 RC SEQUENCE FROM N.A.
 RP MEDLINE=93305725; PubMed=8318540;
 RA Lim J.-K., Langer J.A.;
 RT "Cloning and characterization of a bovine alpha interferon receptor."
 RL Biochim. Biophys. Acta 1173:314-319(1993).
 CC -1- FUNCTION: Receptor for interferons alpha and beta. Binding to type
 CC I IFNs triggers tyrosine phosphorylation of a number of proteins
 CC including JAKs, TYK2, STAT proteins and IFNAR alpha- and beta-
 CC subunits themselves.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the type II cytokine family of receptors.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; X68443; CAA48484.1; -
 CC EMBL; L06320; AAA02571.1; -
 CC PIR; S27387; S27387.
 CC InterPro; IPR000282; Cytok receptor_2.
 CC InterPro; IPR008957; FN_III-like.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR001187; Tissue_factor.

Pfam; PF01108; Tissue_fac; 1.
 DR SMART; SMO0060; FN3; 2.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 560
 FT INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT CHAIN.
 FT DOMAIN 25 437
 FT TRANSMEM 438 458
 FT DOMAIN 459 560
 FT DISULFID 76 84
 FT DISULFID 199 220
 FT CARBOHYD 47 47
 FT CARBOHYD 55 55
 FT CARBOHYD 85 85
 FT CARBOHYD 109 109
 FT CARBOHYD 172 172
 FT CARBOHYD 254 254
 FT CARBOHYD 313 313
 FT CARBOHYD 377 377
 FT CARBOHYD 434 434
 FT CONFLICT 422 422
 SQ SEQUENCE 560 AA; 63818 MW; 66D76B72861E1D11 CRC64;
 Query Match: 10.8%; Score 134.5; DB 1; Length 560;
 Best Local Similarity 23.8%; Pred. No. 4.8e-05;
 Matches 45; Conservative 34; Mismatches 89; Indels 21; Gaps 7;
 QY 29 TPQKVRFSORNFHILHWQAGSSLPNSNYSFYQY-----KMYG--QSQWEDKVDWCWT 80
 DB 231 SPENIQINADNQIYVLKW----DYPENATFOQWLRAFFKIPGNHSDKWKQIPNCENV 286
 QY 81 TALFCDLITNETLDPYELYIGRWMTACAGRHSAWTRTPRTPWETKLDPPVVTITRV-NA 139
 DB 287 TSHCVFPRE-VSSRGIIYVVRASNGNGTSFWSBEKEFNTEMTKTIIFPPVISVKSVTDD 345
 QY 140 SLRVLLRPPPLPNRQSGKASMETYGLVYRVFTTNNLSLEKQAYEGTQRAVEIGLI 199
 DB 346 SLHVSV-----GASEESENMSVQLYPLIYVIFWENTSNAERKYLEKRTNFI-PPDLK 398
 QY 200 PHSSYCVVA 208
 DB 399 PLTVYCVKA 407
 RESULT 15
 INR2_BOVIN STANDARD; PRT; 530 AA.
 ID INR2_BOVIN
 AC Q95141;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interferon-alpha/beta receptor beta chain precursor (IFN-alpha-REC)
 DE (Type I interferon receptor) (IFN-R) (interferon alpha/beta receptor-
 DE 2).
 GN IFNAR2 OR IFNARB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Endometrium;
 RX MEDLINE=98006425; PubMed=9348203;
 RA Han C.-S., Nathalagan N., Klemann S.W., Roberts R.M.;
 RT "Molecular cloning of ovine and bovine type I interferon receptor
 RT subunits from uteri, and endometrial expression of messenger
 RT ribonucleic acid for ovine receptors during the estrous cycle and
 RT pregnancy."
 RL Endocrinology 138:4757-4767(1997).
 CC -1- FUNCTION: Receptor for interferons alpha and beta. Probably
 CC involved in signal transduction by interacting with the tyrosine
 CC kinase, JAK1.

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OM protein - protein search, using sw model

Run on: March 12, 2004, 15:56:12 ; Search time 45 Seconds
(without alignments)
1612.649 Million cell updates/sec

Title: US-10-090-365-48

Perfect score: 1242
Sequence: 1 MPMKCHLGLILLSSATE.....YQPFDRSPSRKRCVHIP 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriapi:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	230	11 Q7TN15	Q7tn15 mus musculu
2	1231	99.1	230	11 Q80XF5	Q80xf5 mus musculu
3	1049	84.5	229	11 Q7TN14	Q7tn14 rattus norv
4	826.5	56.5	231	4 Q96A41	Q96a41 homo sapien
5	800.5	54.5	263	4 Q96A95	Q96a95 homo sapien
6	433.5	34.9	130	4 Q96QR0	Q96qr0 homo sapien
7	285.5	23.0	546	11 Q8BW64	Q8bw64 mus musculu
8	277	22.3	553	4 Q9UHE4	Q9uh4 homo sapien
9	277	22.3	553	4 Q9ESH8	Q9esh8 homo sapien
10	263	21.2	581	11 Q80XZ4	Q80xz4 mus musculu
11	254	20.5	574	4 Q9N6P7	Q9n6p7 homo sapien
12	254	20.5	574	4 Q9HB22	Q9hb22 homo sapien
13	237.5	19.1	209	4 Q9BSH7	Q9esh7 homo sapien
14	215	17.3	203	13 Q7ZT05	Q7zt05 tetraodon n
15	210.5	16.9	568	13 Q80OG1	Q80og1 tetraodon n
16	210.5	16.9	568	13 Q80OF7	Q80of7 tetraodon n

17	186	15.0	569	11 Q99ND6	Q99nd6 rattus norv
18	184.5	14.9	435	13 Q7ZT26	Q7zt26 tetraodon n
19	168	13.5	351	11 Q8VHM7	Q8vhm7 mus musculu
20	163.5	13.2	489	4 Q9BY69	Q9by69 homo sapien
21	158.5	12.8	569	13 Q9YHW0	Q9yhw0 gallus gall
22	156.5	12.6	341	13 Q9YGC8	Q9ygc8 gallus gall
23	155.5	12.5	442	13 Q9PVJ9	Q9pvj9 gallus gall
24	153	12.3	325	4 Q9BUU4	Q9buu4 homo sapien
25	152	12.2	336	13 Q80UE8	Q80ue8 tetraodon n
26	151	12.2	484	4 Q14936	Q14936 homo sapien
27	148	11.9	535	11 Q8CGK5	Q8cgg5 mus musculu
28	147	11.8	338	13 Q80OC2	Q80oc2 tetraodon n
29	145	11.7	508	13 Q9YHV9	Q9yhy9 gallus gall
30	143.5	11.6	211	4 Q8IZI7	Q8izi7 homo sapien
31	143.5	11.6	244	4 Q8IV66	Q8iv66 homo sapien
32	143.5	11.6	491	4 Q8IZI8	Q8izi8 homo sapien
33	143.5	11.6	520	4 Q8IU57	Q8iu57 homo sapien
34	143	11.5	508	13 Q9PVR0	Q9pvk0 gallus gall
35	140	11.3	590	11 Q80UR8	Q80ur8 mus musculu
36	140	11.3	590	11 Q80UJ3	Q80uj3 mus musculu
37	138.5	11.2	294	11 Q8R301	Q8r3d1 mus musculu
38	138.5	11.2	477	11 Q91Y85	Q9ly85 mus musculu
39	137.5	11.1	220	4 Q86SE7	Q86se7 homo sapien
40	137.5	11.1	238	4 Q86WH4	Q86wh4 homo sapien
41	134.5	10.8	464	11 Q9QZ62	Q9qz62 rattus norv
42	131	10.5	301	13 Q7ZT35	Q7zt35 tetraodon n
43	130.5	10.5	294	13 Q90W13	Q90w13 oncorhynch
44	123.5	9.9	239	4 Q15467	Q15467 homo sapien
45	123.5	9.9	331	4 Q9BUA0	Q9buao homo sapien

ALIGNMENTS

RESULT 1

Q7TN15 ID Q7TN15 PRELIMINARY; PRT; 230 AA.

AC Q7TN15; 01-OCT-2003 (TREMREL. 25, Created)
DT 01-OCT-2003 (TREMREL. 25, Last sequence update)
DE Putative cytokine receptor family II soluble 1 precursor.
GN CRP2-S1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RA Gruenberg B.H., Weiss B., Asadullah K., Sabat R.;
RT "Comparison of the human and murine IL-22BP gene leads to differences in gene structure and expression."
RL Submitted (APR-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AJ555484; CAD88474.1; -;
KW Receptor; Signal.
FT SIGNAL 1 18
FT CHAIN 19 230 putative cytokine receptor family II soluble 1.
SQ SEQUENCE 230 AA; 26612 MW; 9AEBB4EDFBAFC105 CRC64;

Query Match 100.0%; Score 1242; DB 11; Length 230;

Best Local Similarity 100.0%; Pred. No. 5.5e-120;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPMKCHLGLILLSSATEIQPARVSLTPQKVRPQSRNFNHLHWAGCSLPSNNSIYF 60

Db 1 MPMKCHLGLILLSSATEIQPARVSLTPQKVRPQSRNFNHLHWAGCSLPSNNSIYF 60

QY 61 VOYKMGQSQWEDKVDGWTGTTALFCDLTNETLDPYELYGRVMTACAGRHSATWTRPFT 120

Db 61 VOYKMGQSQWEDKVDGWTGTTALFCDLTNETLDPYELYGRVMTACAGRHSATWTRPFT 120


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RA Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutsmeier S.,
RA Yao L., Whitmore T.E., Chandrasekhar Y., Grant F.J., Maurer M.,
RA Jelinek L., Storey H., Brander T., Hammond A., Topouzis S.,
RA Clegg C.H., Foster D.C.,
RA "A soluble class II cytokine receptor, IL-22RA2, is a naturally
RA occurring IL-22 antagonist.",
RL Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RA Dmoulier L., Lejeune D., Renaud J.C.;
RA "Cloning and characterization of Interleukin-22 Binding Protein (IL-
RA 22BP), a natural antagonist of IL-TIF/IL-22.",
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ313161; CAC85634.1; -
DR EMBL: AY040566; AAK85714.1; -
DR EMBL: AY044429; AAK91775.1; -
DR EMBL: AJ297262; CAC83097.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR000282; Cytok receptor_2.
DR InterPro: IPR008957; FN_III-like.
KW Receptor; Signal.
FT SIGNAL 1 21
FT CHAIN 22 231
FT FT
SQ SEQUENCE 231 AA; 26979 MW; 24A6912BFF75100F CRC64;
Query Match 66.5%; Score 826.5; DB 4; Length 231;
Best Local Similarity 66.7%; Pred. No. 4.7e-77;
Matches 154; Conservative 20; Mismatches 56; Indels 1; Gaps 1;
Qy 1 MNPKHCLLGLLI-ILLSSATIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPSNNSIY 59
Db 1 MNPKHCFGLFLISFLTGVAGTQSTHESLKPQVQFQSRNFHNLQWQGRALTGNSVY 60
Qy 60 FVQYKMGQSQWEDKVCDCWGTALFCDLNTETLPVELYGRVMTACAGHSAWTRPRF 119
Db 61 FVQYKMGQSQWEDKVCDCWGTALFCDLNTETLPVELYGRVMTACAGHSAWTRPRF 120
Qy 120 TPWNETKLDPPVVTITRVNASLRLVLPPELNPQSGKNASMETYVGLVRYFTINNSL 179
Db 121 TPWNETKIDPPVMTITQVNSLLVILHAPNLPYQKQKNSIEDYVGLVRYFTINNSL 180
Qy 180 EKEQKAYGTORAVEIEGLIPHSYCVVAEMYPMDRRSPRSKRCVHIP 230
Db 181 EKEQKAYGTORAVEIEALTPHSSYCVVAETIYQPMIDRRSQSRSEECVHIP 231
RESULT 5
Q969J5 PRELIMINARY; PRT; 263 AA.
AC Q969J5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Soluble cytokine class II receptor, long isoform precursor
DE (Interleukin 22-binding protein CRF2-10L).
GN CRF2-S1 OR IL22BP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=21518574; PubMed=11607789;
RA Gruenberg B.H., Schonenmeyer A., Weiss B., Toschi L., Kunz S.,
RA Wolk K., Asadullah K., Sabat R.;
RA "A novel, soluble homologue of the human IL-10 receptor with
RA preferential expression in placenta.",
RT Genes Immun. 2:329-334 (2001).
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=21286453; PubMed=11390454;
RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,
RA Dickensheets H., Donnelly R.P., Pestka S.;
RA "Identification, cloning, and characterization of a novel soluble
RA receptor that binds IL-22 and neutralizes its activity.",
RL J. Immunol. 166:7096-7103 (2001).
DR EMBL: AJ313162; CAC85635.1; -
DR EMBL: AY040567; AAK85715.1; -
DR Genew; HGNC:14901; IL22RA2.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR000282; Cytok receptor_2.
DR InterPro: IPR008957; FN_III-like.
KW Receptor; Signal.
FT SIGNAL 1 21
FT CHAIN 22 263
FT FT
SQ SEQUENCE 263 AA; 30550 MW; C96EC5D78AC79B CRC64;
Query Match 64.5%; Score 800.5; DB 4; Length 263;
Best Local Similarity 58.6%; Pred. No. 2.7e-74;
Matches 154; Conservative 20; Mismatches 56; Indels 33; Gaps 2;
Qy 1 MNPKHCLLGLLI-ILLSSATIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPSNNSIY 59
Db 1 MNPKHCFGLFLISFLTGVAGTQSTHESLKPQVQFQSRNFHNLQWQGRALTGNSVY 60
Qy 60 FVQYKMGQSQWEDKVCDCWGTALFCDLNTETLPVELYGRVMTACAGHSAWTRPRF 87
Db 61 FVQYKMGQSQWEDKVCDCWGTALFCDLNTETLPVELYGRVMTACAGHSAWTRPRF 120
Qy 88 TNETLDPVELYGRVMTACAGHSAWTRPRTPWNETKLDPPVVTITRVNASLRLVLP 147
Db 121 TSSETDIOEPYVGRVRAASAGSYSEWSMTPTPTWNETKIDPPVMTITQVNSLLVILHA 180
Qy 148 PELPNRQSGKNASMETYVGLVRYFTINNSLEKEQKAYGTORAVEIEGLIPHSYCVV 207
Db 181 PNLPRYQKQKNSIEDYVGLVRYFTINNSLEKEQKAYGTORAVEIEALTPHSSYCVV 240
Qy 208 AEMYQPMIDRRSPRSKRCVHIP 230
Db 241 ABIYQPMIDRRSQSRSEECVHIP 263
RESULT 6
Q96QR0 PRELIMINARY; PRT; 130 AA.
AC Q96QR0
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 22-binding protein CRF2-10S.
GN IL22BP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286453; PubMed=11390454;
RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,
RA Dickensheets H., Donnelly R.P., Pestka S.;
RA "Identification, cloning, and characterization of a novel soluble
RA receptor that binds IL-22 and neutralizes its activity.",
RL J. Immunol. 166:7096-7103 (2001).
DR EMBL: AY040568; AAK85716.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR InterPro: IPR000282; Cytok receptor_2.
DR InterPro: IPR008957; FN_III-like.
```

SQ SEQUENCE 130 AA; 15128 MW; A165814C641F5E5B CRC64;

Query Match 34.9%; Score 433.5; DB 4; Length 130;
Best Local Similarity 62.4%; Pred. No. 9.2e-37;
Matches 78; Conservative 12; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MNPKECLGLLT-IILSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPSSNRSY 59
Db 1 MNPKECLGLLT-IILSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPSSNRSY 60
Qy 60 FVOYKXGQSQWEDKVDWGTGTTALFCDLTNETLDPYELYYGRVMTACAGRHSAWTRTPRF 119
Db 61 FVOYKIYGRQWKNKEDCWGTQELSDLTSETSDIPEYGRVRAASAGSYSEWSMTPRF 120
Qy 120 TPWE 124
Db 121 TPWE 125

RESULT 7

Q8BM64 PRELIMINARY; PRT; 546 AA.

AC Q8BM64; (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to BA204P2.1.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK054215; BAC35695.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR000282; Cytochrome_2.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR001187; Tissue factor.
DR Pfam; PF01108; Tissue_fac; 1.
SQ SEQUENCE 546 AA; 61978 MW; E7EC07DA2D49AF7F CRC64;

Query Match 23.0%; Score 285.5; DB 11; Length 546;
Best Local Similarity 31.9%; Pred. No. 1.1e-20;
Matches 73; Conservative 31; Mismatches 118; Indels 7; Gaps 4;

Qy 3 PKHCLGLLT-IILSSATEIQPARVSLTPQKVFQSRNFHNLHWQAGSSLPSSNRSY 61
Db 15 PELLTLLTLLAASGRAVPCVCGPLKPTNITFLSINMKNVLMNPPSLHGVETVTV 74
Qy 62 QYKXGQSQWEDKVDWGTGTTALFCDLTNETLDPYELYYGRVMTACAGRHSAWTRTPRF 121
Db 75 QYFYGQKWLNASKCSINRTYCDLSVETSDYEHQFYAKVKAWEARCEWATERFYP 134
Qy 122 WWTETKLPVPVVTITRVNASLRLRPPELNNQSGKNASMETYY-GLVYRVFTINNSLE 180
Db 135 FLETQVSPPEVALTTGKSIISALTAPKWKRPQDHTVSMQOIYPNLKYNSVYNT--- 191
Qy 181 KEQKAYEG--TORAVEIEGLIPHSYCVVAMQPMFDRSPRSKERC 227
Db 192 KSRRTWSQCVNTSTLVSLWLEPNTLYCHVESLVPGPRLPMPQKQCI 240

RESULT 8

Q9UHF4 PRELIMINARY; PRT; 553 AA.

AC Q9UHF4; (TREMBlrel. 13, Created)
DT 01-MAR-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Class II cytokine receptor ZCYTOR7.
GN ZCYTOR7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Kho C., Jellberg A., Adams R., Whitmore T., Farrah T.,
O'Hara P.;
RT "Homo sapiens cytokine receptor homolog."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
Martinez T., Hoffman R., O'Hara P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184971; AAF01320.1; --
DR HSP; P13726; 2HT.
DR Genew; HGNC:6003; IL20RA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR000282; Cytochrome_2.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR001187; Tissue factor.
DR Pfam; PF01108; Tissue_fac; 1.
KW Receptor.
SQ SEQUENCE 553 AA; 62533 MW; 7C23C8543B114659 CRC64;

Query Match 22.3%; Score 277; DB 4; Length 553;
Best Local Similarity 32.5%; Pred. No. 8.8e-20;
Matches 65; Conservative 30; Mismatches 99; Indels 6; Gaps 3;

Qy 30 PQKVFQSRNFHNLHWQAGSSLPSSNRSYFVOYKXGQSQWEDKVDWGTGTTALFCDLTN 89
Db 40 PANITFLSINMKNVLMNPPSLHGVETVTVFYQYKXGQSQWEDKVDWGTGTTALFCDLSA 99
Qy 90 ETLDPYELYYGRVMTACAGRHSAWTRTPRFQWETKLPDPVVTITRVNASLRLRPPE 149
Db 100 ETSYEHQYAKVKAWEARCEWATERFYPLEQIGPEVALTTDEKSIISVLTAP 159
Qy 150 LPNNQSGKNASMETYY-GLVYRVFTINNSLEKEQKAYEG--TORAVEIEGLIPHSYCV 206
Db 160 KWKENPEDLPVSMQOIYPNLKYNSVLT---KSNRTWSQCVNTHTLVLTWLEPNTLYCV 216
Qy 207 VAEYQPMFDRSPRSKERC 226
Db 217 HVESFVGPFPARRAQPSKQC 236

RESULT 9

Q96SH8 PRELIMINARY; PRT; 553 AA.

AC Q96SH8; (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE BA204P2.1.1 (Interleukin 20 receptor alpha, isoform 1).
GN IL20RA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Griffiths C.;

```

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL135902; CAC38375.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004896; F: hemopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004892; F: receptor activity; IEA.
DR GO; GO:0007596; P: blood coagulation; IEA.
DR GO; GO:000282; C: cytokine receptor_2.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF01108; Tissue_fac; I.
DR Receptor.
SQ SEQUENCE 553 AA; 62485 MW; D5C2621FDC848328 CRC64;

Query Match 22.3%; Score 277; DB 4; Length 553;
Best Local Similarity 32.5%; Pred. No. 8.8e-20;
Matches 65; Conservative 30; Mismatches 99; Indels 6; Gaps 3;

QY 30 PQKVFQSRNFHNLHWQAGSSLPNSNLSIFVQYKMGQSQWEDKVDGCTTALFCDLTN 89
DB 40 PANITFSLINKNVQLWTPPEGLQGVKTYTVQYFIYQKKWLKNSCRNINRTYCDLSA 99
QY 90 ETLDPYELYYGRVMTACAGHSAWTRTPFTFWETKLDPPVVTITRVNASLRVLLAPPE 149
DB 100 ETSDEHQYAKVAKAIWTKCKWAESGRFFYLETQIGPEVALTTDEKSIISVLTAPE 159
QY 150 LPNRNOSGKNASMETYY-GLVYRVFTINNSLEKEQKAYEG--TORAVEIEGLIPHSSYCV 206
DB 160 KWKRNPEPLPVMQOIVSNLKNYSVLNT---KSNRTWSQCVTNHTLVLTWLEPNTLYCV 216
QY 207 VAEYQPMFDRSPRSKERC 226
DB 217 HVESFVPGPPRAQPSERQOC 236

RESULT 10
ID Q80XZ4 PRELIMINARY; PRT; 581 AA.
AC Q80XZ4;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-22 receptor alpha chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=22505377; PubMed=12618864;
RA Tachibana A., Imamura R., Wang Y., Fukui M., Umehara M., Suda T.;
RT "Genomic structure and inducible expression of the IL-22 receptor
alpha chain in mice."
RL Genes Immun. 4:153-159(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RA Aiko T., Wang Y., Suda T.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY103454; AAM52222.1; -.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0004896; F: hemopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004892; F: receptor activity; IEA.
DR InterPro; IPR000282; Cytokine receptor_2.
DR InterPro; IPR008957; FN_III-like.
DR Receptor.
SQ SEQUENCE 581 AA; 63794 MW; A2BF8692BB8AA93B CRC64;

Query Match 21.2%; Score 263; DB 11; Length 581;
Best Local Similarity 33.0%; Pred. No. 2.6e-18;
Matches 63; Conservative 34; Mismatches 88; Indels 6; Gaps 4;

QY 31 QKVRFSQSRNFHNLHWQAGSSLPNSNLSIFVQYKMGQSQWEDKVDGCTTALFCDLTN 90
DB 26 QHVFKQSSNFENILTWGGPA-STSDTVSYVEYKYGKRLAKAGCQRITQKFCNLIME 84
QY 91 TLDPYELYYGRVMTACAGHSAWTRTPFTFWETKLDPPVVTITRVNASLRVLLAPPEL 150
DB 85 TRNHTFYAKVTAVSAGPPVTKMTDFPSLQHTTIKFPDVTCTPKVRSIQMLVHPTLT 144
QY 151 PNRNOSGKNASMETYYGLVYRVFTINNSLEKEQKAYEGTORAVEIEGLIPHSSYCVVA 208
DB 145 PVLSEGDGHQLTEIEIFHDLFVRLHVNHTY---QMHLEKQREYEFGLTPTDFEFLGSI 201
QY 209 ENYQPMFDRRS 219
DB 202 TITFILSKES 212

RESULT 11
ID Q8N6P7 PRELIMINARY; PRT; 574 AA.
AC Q8N6P7;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin 22 receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal cortex;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029273; A8H29273.1; -.
DR Genew; HGNC:13700; IL22RA1.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0004896; F: hemopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004892; F: receptor activity; IEA.
DR InterPro; IPR000282; Cytokine receptor_2.
DR InterPro; IPR008957; FN_III-like.
DR Receptor.
SQ SEQUENCE 574 AA; 63076 MW; D46CC71D496F3420 CRC64;

Query Match 20.5%; Score 254; DB 4; Length 574;
Best Local Similarity 32.5%; Pred. No. 2.2e-17;
Matches 69; Conservative 31; Mismatches 106; Indels 6; Gaps 4;

QY 10 LLIILLSSATEIQPARVSLTPQKVRFSQSRNFHNLHWQAGSSLPNSNLSIFVQYKMGQSQ 69
DB 5 LTLTIVGSLAAHAPEDPSDLLGHVQFSNFNILTWDSGPB-GTPDVTYSIEYKTYGER 63
QY 70 QWEDKVDGCTTALFCDLTNLTDPYELYYGRVMTACAGHSAWTRTPFTFWETKLDLP 129
DB 64 DWVAKKGCQRITRKSCNLTVEGTNLTLYYARVAVSAGRSATKMTDRFSSLOHTTLKP 123
QY 130 PVVTITRVNASLRVLLAPPELNRNOSGKNASMETYYGLVYRVFTINNSLEKEQKAYE 187
DB 124 PDVTCISKVRSIQMLVHPTTPIRAGDGHRLTDFHDLFVHLELVNRY---QMHLG 180
QY 188 GTORAVEIEGLIPHSSYCVVAENYQPMFDRRS 219
DB 181 GKQREYEFGLTPTDFEFLGIMICVPTWAKES 212

RESULT 12
ID Q9HB22 PRELIMINARY; PRT; 574 AA.
AC Q9HB22;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE IL-22 receptor.
GN IL22R.
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OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RX [1]
 RN
 PP SEQUENCE FROM N.A.
 RZ MEDLINE=20469498; PubMed=10875937;
 RA Xie M.H., Aggarwal S., Ho W.H., Foster J., Zhang Z., Stinson J.,
 RA Wood W.I., Goddard A.D., Gurney A.L.;
 RA "Interleukin (IL)-22, a Novel Human Cytokine That Signals through the
 RPT Interferon Receptor-related Proteins CRF2-4 and IL-22R.";
 RPT J. Biol. Chem. 275:31335-31339(2000).
 RRL
 RLL EMBL; AF286095; AAG22073.1; -.
 DR HSP; P13726; 1TFH.
 DR GO; GO:0016020; C:membrane; NAS.
 DR GO; GO:0004904; F:interferon receptor activity; TAS.
 DR InterPro; IPR000282; Cytok receptor_2.
 DR InterPro; IPR008957; FN_III-like.
 DR Receptor.
 KW Receptor.
 SQ
 SEQUENCE 574 AA; 62977 MW; C179C7085C6F3420 CRC64;
 Query Match 20.5%; Score 254; DB 4; Length 574;
 Best Local Similarity 32.5%; Pred. No. 2.2e-17;
 Matches 69; Conservative 31; Mismatches 106; Indels 6; Gaps 4;
 QY 10 LAILLSSATEIQPARVSLTPQKVRFSQRFNHILHWAGSSLPNSNIYFVQKMGOS 69
 DB 5 LILTVGSLAAHAPDPSDLLQHVKQSSNFENILTWDSQPE-GTPTVYSIEYKTYGER 63
 QY 70 QNEDKVDVCGTTTALFCDLTNELDPVELYYGYRVMTACAGHSASWTPTPTPWETKLD 129
 DB 64 DWAKKGQCORITKSKNLTVETGNLTLEYIYRVTAVSAGRSATKMTDRFSLQHTLKP 123
 QY 130 PVVTIIRVNASLRVLRPELPNRNSGKNASME-TYVGLVYRV-FTNNSLEKEQAYE 187
 DB 124 PVTCTSKRSIQNIHVHTPTTPRAGDCHRLTIEDIFHDLFYHLEQVARTY---QMHLG 180
 QY 188 GTQRAVEIEGLPHSSYCVVAEMYQPMFDRRS 219
 DB 181 GKQREYEFFGLTPTDTEPLGTIMICVPTWAKES 212
 RESULT 13
 Q96SH7
 ID Q96SH7 PRELIMINARY; PRT; 209 AA.
 AC Q96SH7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE B2A04P2.1.3 (Interleukin 20 receptor alpha, isoform 3).
 GN IL20RA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RX [1]
 RN
 PP SEQUENCE FROM N.A.
 RZ Griffiths C.
 RA Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AL335902; CAC38376.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004836; F:hematopoietin/interferon-class (D200-domain. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000282; Cytok receptor_2.
 DR InterPro; IPR008957; FN_III-like.
 KW Receptor.
 SQ
 SEQUENCE 209 AA; 23616 MW; 467AB77BE3840361 CRC64;
 Query Match 19.1%; Score 237.5; DB 4; Length 209;
 Best Local Similarity 31.8%; Pred. No. 3e-16;
 Matches 57; Conservative 22; Mismatches 87; Indels 13; Gaps 3;
 QY 30 POKYRFQSRNFHNLHWAGSSLPNSNIYFVQKMGOSQWEDKVCWGTTALFCDLTN 89

Db	40	PANITFUSLNNKKNVLQWTFPEGLQGVKVTYTVQYFIYGQKKWLKSECRNINRTYCDLSA	99
Qy	90	ETLDPYELYGRYNTACAGHSAWTEPRFTPWETKLDPPVVTITRVNASLRLVRPPE	149
Db	100	ETSDYEQYAKVKAIMGTKSCSWAESGRFYFPLETQGPPEVAULTDEKISVVLTAPE	159
Qy	150	LPNENQSGKNASMETYY-GLAVYRVFTINNSLEKEQKAYEGTORAVEIE--GLIPHSYSYC	205
Db	160	KWKNRPEDLPVSMQOIVSNLKNVSVLNTK-----SNRTVSLKWNGAYIHPPLC	208
RESULT 14			
Q72T05			
ID	Q72T05	PRELIMINARY;	PRT; 203 AA.
DT	01-JUN-2003	(TrEMBLrel. 24, Created)	
DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Helical cytokine receptor CRFB9.		
GN	CRFB9.		
OS	Tetraodon nigroviridis (Green puffer).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		
OC	Tetraodontidae; Tetraodontidae; Tetraodon.		
OX	NCBI_TaxID=99983;		
ON	[1]		
RE	SEQUENCE FROM N.A.		
RP	Lutalla G.; Roest Crolius H.; Stange-Thomann N.; Jaillon O.;		
RA	Mogensen K.; Monneron D.;		
RA	"Comparative genomic analysis reveals independent expansion of a		
RT	lineage-specific gene family in vertebrates: The class II cytokine		
RT	receptors and their ligands in mammals and fish.";		
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.		
RP	[2]		
RE	SEQUENCE FROM N.A.		
RP	Lutalla G.;		
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ544912; CAD67770.1; --		
DR	EMBL; AJ544895; CAD67783.1; --		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . . ; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
KW	InterPro; IPR000282; Cytok_receptor_2.		
KW	Receptor.		
SEQ	SEQUENCE 203 AA; 22779 MW; 9F1E843FA4E75E82 CRC64;		
Query Match 17.3%; Score 215; DB 13; Length 203;			
Best Local Similarity 29.3%; Pred.No. 6.2e-14;			
Matches 65; Conservative 33; Mismatches 90; Indels 34; Gaps 7			
Qy	8	LGILLILSSATEIQPARVSLTPQKVFQSRNFHILHWQAGSLSPNNS--ZYFVQYKM 65	
Db	11	LGTLGLGAGVDLAP-----PTNLAFDSVDYKNVLSW---SPFANGSSLLYDVQWKI 60	
Qy	66	YQGSQWEKVDWGHTALFCDLTNETLDPYLYYGRVNTACAGHSAWTEPRFTPWET 125	
Db	61	YGDPPWLDAASCRCGQKLCRDLSSSETSVPREYYARFVITA-----PHTP-----AA 108	
Qy	126	KLDPPPVVITRVNASLRLVLLPPLPNRNSGKNASMETYYGLYRVFTINNSLEKEQA 185	
Db	109	RISPPVVLKYSQKVVVVQVEPPRLHIA-----KHSLLQFKLYLTHPSGEELFL 159	
Qy	186	YEGTQRAVEIEGLIPHSYSYCVVAEMYPMPDRSPRSKERCY 227	
Db	160	VDPRSKTLIH-LRHRQRYCQVQAQFILLQAKSARSPTTCV 200	

RESULT 15
Q800G1
ID Q800G1 PRELIMINARY; PRT; 568 AA.
AC Q800G1;

Query Match 19.1%; Score 237.5; DB 4; Length 209;
Best Local Similarity 31.8%; Pred. No. 3e-16;
Matches 57; Conservative 22; Mismatches 87; Indels 13; Gaps 3;
30 POKVRFOSNFNNILHWAGSSLPNNSTIFYOYRWYGOSOWEDKVCWGWTALFCSLLTN 89

